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9/6 02

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SEARCH REQUEST FORM
Scientific and Technical Information Center

Requester's Full Name: Nimal S. Bosi Examiner #: _____ Date: 9/5/02
Art Unit: _____ Phone Number 30 89435 Serial Number: 09/827937
Mail Box and Bldg/Room Location: CM1 10E17 Results Format Preferred (circle): PAPER DISK E-MAIL
Mail room 10019

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: Human G-Protein coupled Receptor
Inventors (please provide full names): Li et al

Earliest Priority Filing Date: 5/7/97

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Mean search
1 SEQ ID NO: 2

Point of Contact:
Toby Port
Technical Info. Specialist
CM1 6A04
703-308-3534

Unmerged + issued + interference data base

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Prot 2

STAFF USE ONLY		Type of Search	Vendors and cost where applicable
Searcher: _____	NA Sequence (#) <u>1</u>	STN _____	
Searcher Phone #: _____	AA Sequence (#) _____	Dialog _____	
Searcher Location: _____	Structure (#) _____	Questel/Orbit _____	
Date Searcher Picked Up: <u>9/3</u>	Bibliographic _____	Dr.Link _____	
Date Completed: <u>9/9</u>	Litigation _____	Lexis/Nexis _____	
Searcher Prep & Review Time: <u>12</u>	Fulltext _____	Sequence Systems <u>AS</u>	
Clerical Prep Time: _____	Patent Family _____	WWW/Internet _____	
Online Time: <u>12</u>	Other _____	Other (specify) _____	

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 6, 2002, 15:27:51 ; Search time 32.67 Seconds
(without alignments)
1152.756 Million cell updates/sec

Title: US-09-827-937A-2
Perfect score: 1778
Sequence: 1 MQAVDNLTSAPGNTSLCTRD.....SODNRKKEDGGDPEETPM 342

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_032802:*

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- 2: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT.*
- 3: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT.*
- 4: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1983.DAT.*
- 5: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1984.DAT.*
- 6: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1985.DAT.*
- 7: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1986.DAT.*
- 8: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1987.DAT.*
- 9: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1988.DAT.*
- 10: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1989.DAT.*
- 11: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1990.DAT.*
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- 16: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1995.DAT.*
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- 18: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1997.DAT.*
- 19: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT.*
- 20: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT.*
- 21: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.*
- 22: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1778	100.0	342	20	AAW81576
2	1778	100.0	342	21	AAV71306
3	1778	100.0	342	21	AAW02840
4	1778	100.0	342	21	AAV94444
5	1778	100.0	342	22	AAW79249
6	1778	100.0	342	22	AAE04386
7	1748	98.3	342	21	AAV94445
8	1634	91.9	315	22	AAE04385
9	1528.5	86.0	343	22	AAE04384
10	1493.5	84.0	387	21	AAV94498
11	1237.5	69.6	267	22	AAE04387

12	829	46.6	333	21	AAW23029	Human chemokine re
13	829	46.6	333	22	AAW74397	Human G protein co
14	829	46.6	333	22	AAW74494	Novel human G prot
15	827	46.5	333	22	AAE02494	Human CON203 G pro
16	823	46.3	333	20	AAV02171	Human 7-transmembr
17	823	46.3	333	21	AAV71299	Human orphan G pro
18	823	46.3	333	21	AAW02833	Human G protein co
19	823	46.3	333	22	AAU10588	Human HNEA81 poly
20	823	46.3	333	22	AAW31580	Amino acid sequenc
21	810.5	45.6	336	22	AAW62472	Rat 7-transmembran
22	797	44.8	333	19	AAW77322	Human chemokine re
23	792	44.5	337	22	AAW73464	Mouse G protein-co
24	772	43.4	338	21	AAV58237	Human KIAA0001 rec
25	772	43.4	338	22	AAE04388	Human UDP-glucose
26	769	43.3	338	21	AAV97541	Rat KIAA0001 prote
27	741.5	41.7	338	21	AAV94270	Mouse 7-transmembr
28	725	40.8	336	22	AAW12200	Human EBV-induced
29	725	40.8	166	22	AAW80223	Human protein SEQ
30	699.5	39.3	358	22	AAW4659	Human protein sequ
31	699.5	39.3	358	22	AAW85890	Human C-PLACE10032
32	694.5	39.1	358	21	AAV45039	Human G protein-co
33	694.5	39.1	358	21	AAV44365	Human G-protein co
34	694.5	39.1	358	22	AAE03189	Human G-protein co
35	694.5	39.1	358	22	AAE02439	Human CON215 G pro
36	694.5	39.1	358	22	AAW96884	Human novel G-prot
37	694.5	39.1	358	22	AAW83014	Human G protein co
38	694.5	39.1	358	22	AAW67484	Amino acid sequenc
39	687.5	38.7	384	22	AAW84205	Amino acid sequenc
40	679.5	38.2	358	20	AAV28280	Human G-protein co
41	673.5	37.9	358	22	AAW60692	Human G protein-co
42	584	32.8	119	20	AAV11396	Human 5' EST seque
43	546.5	30.7	293	17	AAW04246	Human G-protein co
44	546.5	30.7	293	21	AAW15412	Human G-protein co
45	546.5	30.7	293	21	AAV67355	Human G-protein co

ALIGNMENTS

RESULT 1	AAW81576	standard; Protein: 342 AA.
ID	AAW81576;	
AC	AAW81576;	
XX		
DT	22-FEB-1999	(first entry)
XX		
DE	EBV-induced G-protein coupled receptor (EBI-2) polypeptide.	
XX		
KW	EBV-induced G-protein coupled receptor; EBI-2; Epstein-Barr Virus; ulcer;	
KW	endothelium-differentiation gene; EDG-1-like G-protein coupled receptor;	
KW	recombinant; agonist; asthma; Parkinson's disease; heart failure; asthma;	
KW	hypotension; urinary retention; osteoporosis; antagonist; hypertension;	
KW	angina pectoris; myocardial infarction; allergy; psychosis; depression;	
KW	migraine; vomiting; stroke; eating disorder;migraine headache; cancer;	
KW	prostatic hypertrophy; detection; drug screening.	
XX		
OS	Homo sapiens.	
XX		
FT	Key	Location/Qualifiers
FT	Misc-difference 6	/note= "encoded by AT1"
FT	Misc-difference 14	/note= "encoded by AAC"
FT		
XX		
PN	W09850549-A2.	
XX		
PD	12-NOV-1998.	
XX		
PF	07-MAY-1998;	98W0-US09048.
XX		
PR	07-MAY-1997;	97US-0852824.
XX		

PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Li Y, Ruben SM;
 XX
 DR WPI: 1999-034722/03.
 DR N-PSDB: AAV69760.
 XX
 XX New isolated human G-protein coupled receptors - used to develop
 PT products for treating e.g. asthma, Parkinson's disease, heart
 PT failure, osteoporosis, hypertension, psychoses, eating disorders or
 PT cancers
 PS Claim 1: Fig 1A-C; 65pp; English.
 CC This represents a EBV-induced G-protein coupled receptor (EBI-2)
 CC polypeptide. The encoding DNA is deposited under the accession number
 CC ATCC No: 209003. The invention provides two human G-protein coupled
 CC receptor polypeptides. The polypeptides are human Epstein-Barr Virus
 CC (EBV)-induced G-protein coupled receptor, designated EBI-2 polypeptide
 CC and a human endothelium-differentiation gene (EDG) like G-protein coupled
 CC receptor, designated EDG-1-like G-protein coupled receptor. Vectors
 CC comprising the EBI-2 and EDG-1-like polypeptides encoding DNA can be used
 CC to transform host cells for the recombinant production of the proteins.
 CC Agonists for G-protein coupled receptors can be used for the treatment of
 CC asthma, Parkinson's disease, acute heart failure, hypotension, urinary
 CC retention and osteoporosis. Antagonists can be used for the treatment of
 CC hypertension, angina pectoris, myocardial infarction, ulcers, asthma,
 CC allergies, psychoses, depression, migraine, vomiting, stroke, eating
 CC disorders, migraine headaches, cancer and benign prostatic hypertrophy.
 CC The products can also be used for detection, diagnosis and drug
 CC screening.
 CC
 CC Sequence 342 AA:
 SQ
 Query Match 100.0%; Score 1778; DB 20; Length 342;
 Best Local Similarity 100.0%; Pred. No. 4.2e-187;
 Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX
 KW Human; orphan G protein-coupled receptor; GPCR; hCHN8; drug screening;
 KW transmembrane receptor; expressed sequence tag; EST; signal cascade.
 XX
 OS Homo sapiens.
 XX
 PN WO200031258-A2.
 XX
 PD 02-JUN-2000.
 XX
 PR 13-OCT-1999; 99WO-US23687.
 XX
 PR 20-NOV-1998; 98US-0109213.
 PR 16-FEB-1999; 99US-0120416.
 PR 26-FEB-1999; 99US-0121852.
 PR 12-MAR-1999; 99US-0123946.
 PR 12-MAR-1999; 99US-0123949.
 PR 28-MAY-1999; 99US-0136436.
 PR 28-MAY-1999; 99US-0136437.
 PR 28-MAY-1999; 99US-0136439.
 PR 28-MAY-1999; 99US-0136567.
 PR 28-MAY-1999; 99US-0137127.
 PR 28-MAY-1999; 99US-0137131.
 PR 29-JUN-1999; 99US-0141448.
 PR 29-SEP-1999; 99US-0156553.
 PR 29-SEP-1999; 99US-0156633.
 PR 29-SEP-1999; 99US-0156634.
 PR 29-SEP-1999; 99US-0156653.
 PR 01-OCT-1999; 99US-0157280.
 PR 01-OCT-1999; 99US-0157281.
 PR 01-OCT-1999; 99US-0157282.
 PR 01-OCT-1999; 99US-0157293.
 PR 01-OCT-1999; 99US-0157294.
 PR 12-OCT-1999; 99US-0416760.
 PR 12-OCT-1999; 99US-0417044.
 XX
 PA (AREN-) ARENA PHARM INC.
 PA
 PI Chen R, Dang HT, Liaw CW, Lin I;
 XX
 DR WPI: 2000-400068/34.
 DR N-PSDB: AAD01133.
 XX
 PT Novel human orphan G protein-coupled receptors and the encoding cDNAs
 PT for use in the identification of G protein-coupled receptor agonists -
 XX
 PS Claim 62; Page 82-83; 102pp; English.
 XX
 CC The present amino acid sequence is the hCHN8, an endogenous human
 CC orphan G protein-coupled receptor (GPCR), expressed in left and right
 CC cerebellum, kidney and lung. The hCHN8 cDNA was identified using full
 CC length EST (expressed sequence tag) 764455 as a probe.
 CC The orphan GPCR of the invention, like all GPCRs has seven transmembrane
 CC alpha helices with an extracellular N-terminus and an intracellular
 CC C-terminus. However, no endogenous ligands has yet been identified for
 CC the proteins of the invention. The orphan GPCRs may be used in the
 CC identification of their endogenous ligands, and to screen potential GPCR
 CC agonists and antagonists for use as pharmaceutical agents. The proteins
 CC may also be used in the study of GPCR-mediated signaling cascades, and
 CC to elucidate their precise role in normal and diseased human conditions.
 CC Nucleic acid encoding human orphan GPCRs may be used for tissue
 CC localisation expression analysis to provide information about their
 CC function in healthy and pathological states.
 CC
 CC Sequence 342 AA:
 SQ
 Query Match 100.0%; Score 1778; DB 21; Length 342;
 Best Local Similarity 100.0%; Pred. No. 4.2e-187;
 Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

FT	Misc-difference	/label- N-glycosylation
FT	13	/note- "encoded by ACC"
FT	Modified-site	13..16
FT	Domain	/label- N-glycosylation
FT	26..302	
FT	Modified-site	/label- Transmembrane_domain
FT	39..44	
FT	Modified-site	/label- N-myristoylation
FT	121..123	
FT	Modified-site	/label- GPCR signal transduction site
FT	126..128	
FT	Modified-site	/label- protein_kinase_C_phosphorylation
FT	163..165	
FT	Modified-site	/label- protein_kinase_C_phosphorylation
FT	173..176	
FT	Modified-site	/label- protein_kinase-phosphorylation
FT	303..342	
FT	Domain	/label- Intracellular_domain
FT	304..306	
FT	Modified-site	/label- protein_kinase_C_phosphorylation
FT	333..338	
FT	Modified-site	/label- N-myristoylation
PN	WO200028028-A1.	
PD	18-MAY-2000.	
XX		
XX	05-NOV-1999;	99WO-US25956.
XX	06-NOV-1998;	98US-0187134.
XX	25-AUG-1999;	99US-0382918.
XX		
PA	(MILL-) MILLENNIUM PHARM INC.	
PI	Glucksmann MA, Gu W, Welch NS;	
XX		
DR	WPI: 2000-376543/32.	
XX	N-PSDB: AAA27126.	
PT	Identifying an agent modulating the level or activity of G-protein coupled receptor useful for screening a cell derived from a subject having disorders such as anaemia, neutropenia and thrombocytopenia	
PS	Disclosure: Page 88-89; 97pp: English.	
XX		
XX	The present sequence shows the 15625 receptor protein. It is a novel G-coupled protein receptor (GPCR). The cDNA for this protein was isolated by screening a human cDNA library with sequences homologous to other GPCRs. The 15625 receptor protein is expressed in the glial cells of the brain. It is also expressed in several other tissues. The 15625 receptor protein may be useful for producing antibodies which can be used to detect the presence of the receptor protein. The 15625 receptor protein polynucleotides are useful for generating probes, primers and antisense constructs. The polynucleotides encoding the 15625 receptor proteins can also be inserted into vectors to be used in gene therapy. The disorder that may be treated using the 15625 receptor protein polynucleotides and polypeptides include anaemia, neutropenia and thrombocytopenia.	
XX		
XX	Sequence 342 AA;	
XX		
XX	Query Match	100.0%; Score 1778; DB 21; Length 342;
XX	Best Local Similarity	100.0%; Pred. No. 4, 2e-187;
XX	Matches 342; Conservative	0; Mismatches 0; Indels 0; Gaps
OY	1	MOADVNLISAGCNTSLICRDYKITOVLEPLLYTVLFFVGLITNGLAMRIFPOIRKSNFI 60
Db	1	mgadvnltsapngslscrdykitqivlfpillytvrlffgltlnglamriffgtsksnfi 60
OY	61	IFLKNFTVLSDLMLITPFPKILSDAKIGTGPLRFPVCOVTSVIFFTMYISISPLGLITI 120

Db	61	ifLkhtvtsdIlmIltfckIIsdakIlgcprltfcvcqvsvfifemyIsIsflgItt	120
Oy	121	DKYQKTRTREFKSNRPNNLGGAKILSVYIAFMFLISLPNNILNRRQPRDKNWKCSPLKS	180
Db	121	dtYgklttPfkIsnpknllgakiIsvvIaafmllIsIpmlIlntgrdrknvkcstIks	180
Oy	181	EEGLWHEIIVNVCQYIEMINFLIVCYTLITRKELYSRYVTRTGVGKVPKKVNVFEI	240
Db	181	eEglwheIvnyIcqvlfInflIvIvcYtLIkelyrsYrrtrgygkvpkrknvkvfl	240
Oy	241	IIAVFPICVPHFARIPYTLTSOTRVPFQCTAENITLFYKESFLWLTSLAACDPFIYFF	300
Db	241	IlaVfIcIvPhfArIpYtLsqtrvdfQctaenItlfYkEstlWltSlnacIdpFIyff	300
Oy	301	IIKSFENSLISMUKCPNSATSLSDQRRKEQDGDNEEPTM	342
Db	301	IksfEnslIsmlkcPnsatSlSqdrkKeeQgDpneecpm	342
RESULT 5			
AAM79249			
ID	AAM79249	standard: Protein; 342 AA.	
AC	AAM79249;		
DT	06-NOV-2001	(first entry)	
DE	Human protein SEQ ID NO 1911.		
XX	Human; cytokine; cell proliferation; cell differentiation; gene therapy;		
KW	vaccine; peptide therapy; stem cell growth factor; haematopoiesis;		
KW	tissue growth factor; immunomodulatory; cancer; leukaemia;		
XX	nervous system disorder; arthritis; inflammation.		
OS	Homo sapiens.		
XX	WO200157190-A2.		
PN	09-AUG-2001.		
PD			
XX			
PF	05-FEB-2001; 2001WO-US04098.		
XX			
PR	03-FEB-2000; 2000US-0496914.		
PR	27-APR-2000; 2000US-0560875.		
PR	20-JUN-2000; 2000US-0598075.		
PR	19-JUL-2000; 2000US-0620325.		
PR	01-SEP-2000; 2000US-0654936.		
PR	15-SEP-2000; 2000US-0663561.		
PR	20-OCT-2000; 2000US-0693325.		
PR	30-NOV-2000; 2000US-0728422.		
XX			
PA	(HSE-) HSEQ INC.		
XX			
PI	Tang YN, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;		
PI	Zhao Qh, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;		
PI	Xue AJ, Yang Y, Wejhrman T, Goodrich R.		
XX			
XX	WPI: 2001-476283/51.		
DR	N-PDSB; AAK52382.		
PT			
PT	Nucleic acids encoding polypeptides with cytokine-like activities,		
XX	useful in diagnosis and gene therapy -		
XX			
PS	Claim 20; Page 4310; 6221pp; English.		
XX			
CC	The invention relates to polynucleotides (AAK51456-AAK53435) and the		
CC	encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to		
CC	cytokine, cell proliferation or cell differentiation or which may induce		
CC	production of other cytokines in other cell populations. The		
CC	polynucleotides and polypeptides are useful in gene therapy, vaccines or		
CC	peptide therapy. The polypeptides have various cytokine-like activities,		
CC	e.g. stem cell growth factor activity, haematopoiesis regulating		
CC	activity, tissue growth factor activity, immunomodulatory activity and		

activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukemia, nervous system disorders, arthritis, and inflammation.
 CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666, (AAK60020) are omitted as the relevant pages from the sequence listing were missing at the time of publication.

Query Match 100.0%; Score 1778; DB 22; Length 342;
 Best Local Similarity 100.0%; Pred. No. 4.2e-187; Indels 0; Gaps 0;
 Matches 342; Conservative 0; Mismatches 0;

1 MOAVDNLTSAPGNTSLCTRDYKITQVLEPFLVTFVGLITNGLAMRIFFOIRSKSNFI 60
 1 mqvadnltsapgnslctrdykitqvlepfllvtfvglitnglamrffqirsksnfi 60
 61 IFKNTVTSIDLMITFPFKISDAKLGCPURTFVCQVTSVIFFTWYISIFGLITTI 120
 61 ifkntvtsidlmiltfpfkisdaklgcpurtfvcqvtsvifftwysisifglitl 120
 121 DRYOKTRPFKTSNPKNLGAKILSVYIMAFNELLSPNMLITNRPDRKNVKKCSFLKS 180
 121 dryoktrpfktsnpknlgakilsvyimafnellspnmlltnrpdnkvnkcsflks 180
 181 EFGLVWHEIVNYICOVIFNFIIVCYTLITKELRSYVTRRGVGVPRKKNVKKVFI 240
 181 efglvwheivnyicovifnfiivcytlitkelyrsyvrtrgvgvprkknvkvkfi 240
 241 IIAVFICVFPFHARIPYTLISQTRVFDCTAENTLFYVKESTLWLTSLNACLDPIYTF 300
 241 iiavficvfpfharipytlisqtrvfdctaentlfyvestlwltslnacldpiytf 300
 301 LCKSPRNLISMLKCPNSATSLSDNRRKKEQDGDPEHPEPM 342
 301 lcksprnlismlkcpnsatsslodnrkkekqdgdphepmp 342

RESULT 6
 AA04386
 ID AA04386 standard; Protein: 342 AA.
 AC AA04386;
 DT 04-SEP-2001 (first entry)
 DE Human P2-purinegic receptor subtype, P2Y12.
 XX Human: P2-purinegic receptor; P2Y12; cardiant; vasotropic; thrombolytic;
 KW cerebroprotective; gynaecological; ADP; adenosine 5'-diphosphate; angina;
 KW myocardial infarction; ischaemic attack; preclampsia; bleeding disorder;
 KW myocardial endarterectomy; vascular graft surgery; brain disorder; migraine;
 KW vascular injury; schizophrenia; eating disorder; depression; angiolysis;
 KW peripheral vascular disease; platelet aggregation; restenotic; embolism;
 KW thrombocytopenic purpura; stroke; pertussis toxin sensitive G protein;
 KW G1; disseminated intravascular coagulation; thrombosis.
 XX Homo sapiens.
 OS
 FT Key Location/Qualifiers
 FT 27..50 /label= Transmembrane_domain_1
 FT 58..82 /label= Transmembrane_domain_2
 FT 97..121 /label= Transmembrane_domain_3
 FT 140..163 /label= Transmembrane_domain_4
 FT 189..213 /label= Transmembrane_domain_5
 FT 234..259 /label= Transmembrane_domain_6
 FT Domain

Domain 278..303
 /label= Transmembrane_domain_7
 WO200146454-A1.
 28-JUN-2001.
 26-DEC-2000; 2000WO-US34998.
 23-DEC-1999; 99US-0171622.
 (COR-) COR THERAPEUTICS INC.
 Conley PB, Jantzen H, Ramakrishnan-Dubridge V, Julius DJ;
 Holloper G;
 WPI: 2001-418082/44.
 N-PSDB: AAD08695.
 Novel isolated ADP receptor, termed P2Y12 receptor polypeptide, useful for identifying binding partners and for diagnostic applications -
 Example 1, Fig 5A; 108pp; English.

The invention relates to ADP (adenosine 5'-diphosphate) receptor, termed as P2Y12 receptor and its corresponding cDNA molecule. P2Y12 receptor is the subtype of P2-purinegic receptor. The P2Y12 receptor is expressed selectively in the platelets and brain, and couples to a pertussis toxin-sensitive G protein (Gi). P2Y12 receptor is a G protein-coupled receptor that responds to ADP. The invention also relates to a method for identifying an agent which is useful for modulating acute myocardial infarction, unstable angina, chronic stable angina, transient ischaemic attacks, strokes, peripheral vascular disease, preclampsia, deep venous thrombosis, embolism, disseminated intravascular coagulation, thrombotic cerebrocytopenic purpura or a bleeding disorder; thrombotic and restenotic complications following angioplasty, carotid endarterectomy, CABG (coronary artery bypass graft) surgery, vascular graft surgery, stent placements or insertion of endovascular devices and prostheses. P2Y12 receptor is useful for identifying binding partners and for screening diagnostic small molecules and combinatorial or naturally occurring compound libraries to regulate platelet aggregation, depression, migraine disease as well as schizophrenia, eating disorders, vascular injury, ADP receptor subtype, referred as P2Y12.

Query Match 100.0%; Score 1778; DB 22; Length 342;
 Best Local Similarity 100.0%; Pred. No. 4.2e-187; Indels 0; Gaps 0;
 Matches 342; Conservative 0; Mismatches 0;

1 MOAVDNLTSAPGNTSLCTRDYKITQVLEPFLVTFVGLITNGLAMRIFFOIRSKSNFI 60
 1 mqvadnltsapgnslctrdykitqvlepfllvtfvglitnglamrffqirsksnfi 60
 61 IFKNTVTSIDLMITFPFKISDAKLGCPURTFVCQVTSVIFFTWYISIFGLITTI 120
 61 ifkntvtsidlmiltfpfkisdaklgcpurtfvcqvtsvifftwysisifglitl 120
 121 DRYOKTRPFKTSNPKNLGAKILSVYIMAFNELLSPNMLITNRPDRKNVKKCSFLKS 180
 121 dryoktrpfktsnpknlgakilsvyimafnellspnmlltnrpdnkvnkcsflks 180
 181 EFGLVWHEIVNYICOVIFNFIIVCYTLITKELRSYVTRRGVGVPRKKNVKKVFI 240
 181 efglvwheivnyicovifnfiivcytlitkelyrsyvrtrgvgvprkknvkvkfi 240
 241 IIAVFICVFPFHARIPYTLISQTRVFDCTAENTLFYVKESTLWLTSLNACLDPIYTF 300
 241 iiavficvfpfharipytlisqtrvfdctaentlfyvestlwltslnacldpiytf 300

QY 301 LCKSFNSLSMLKCPNSATSLSDNRKKEODGDPNEETPM 342
 DB 301 lcksfnslsmlkcpnsatslsqdnrkkegdgdpneetpm 342

RESULT 7
 AAY94445
 ID AAY94445 standard; Protein; 342 AA.
 AC AAY94445;
 XX AAY94445;
 DT 21-AUG-2000 (first entry)

DE Macaque ortholog of human 15625 receptor protein.
 XX Human; G-protein-coupled receptor; GPCR; 15625 receptor protein;
 KW glial cells; spleen; colon; liver; brain; T-cell; heart;
 KW red cell; thymus; B-cell; pancreas; disorder; chromosome 3;
 KW anemia; neutropenia; thrombocytopenia; gene therapy; ss.
 OS Macaca sp.
 XX
 FN WO200028028-A1.
 XX
 PD 18-MAY-2000.
 XX
 PF 05-NOV-1999; 99WO-US25956.
 XX
 PR 06-NOV-1998; 98US-0187134.
 PR 25-AUG-1999; 99US-0382918.
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Glucksmann MA, Gu W, Welch NS;
 DR WPI: 2000-376543/32.
 DR N-PSDB; AAA27127.
 XX

PT Identifying an agent modulating the level or activity of G-protein
 PT coupled receptor useful for screening a cell derived from a subject
 XX having disorders such as anaemia, neutropenia and thrombocytopenia
 PS Disclosure: Page 90-92; 97pp; English.
 XX

CC The 15625 receptor protein is a novel G-coupled protein receptor (GPCR).
 CC The cDNA for this protein was isolated by screening a human cDNA library
 CC with sequences homologous to other GPCRs. The 15625 receptor protein is
 CC expressed in the glial cells of the brain. It is also expressed in
 CC several other tissues. The 15625 receptor protein may be useful for
 CC producing antibodies which can be used to detect the presence of the
 CC receptor protein. The 15625 receptor protein polynucleotides are useful
 CC for generating probes, primers and antisense constructs. The
 CC polynucleotides encoding the 15625 receptor protein can also be inserted
 CC into vectors to be used in gene therapy. The disorder that may be
 CC treated using the 15625 receptor protein polynucleotides and
 CC polypeptides include anaemia, neutropenia and thrombocytopenia. The
 CC present sequence is the macaque ortholog of the human 15625 receptor
 CC protein.
 CC
 XX
 XX
 SQ Sequence 342 AA;

Query Match 98.3%; Score 1748; DB 21; Length 342;
 Best Local Similarity 98.0%; Pred. No. 8 3e-184;
 Matches 333; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MQAVNLTSAAGMTSLCTRYKTTQVLFPLVTVLFVGLITNGLAMRFOIRSKSMFI 60
 DB 1 mgaidltsaprtstictaykltqvlfpilytvlffvgiltstamiffqilsksnfi 60
 QY 61 IIFKNVVISDLMLILFPFKILSDAKLGTGPRFVCOVTVIFVFWYISISFLGILTI 120
 DB 61 ifknvvisdlmlilfpfkilsdaklgtgprfvcovtvifvfwyisiflglitl 120
 61 ifknvvisdlmlilfpfkilsdaklgtgprfvcovtvifvfwyisiflglitl 120

QY 121 DRVQKTRPFTKSNPKNLGAKILSVITWAFMFLSLPMLNLNRQDRNKKCSFLKS 180
 DB 121 drvqktrpftkspnknlgakilsvitwafmflslpmlnlnrprdknvkcsflks 180
 QY 181 EFGIWWHEIVANICOVTFWINEFLVIVCYLTITKELRSYVTRGVGKPRKVNKVI 240
 DB 181 efgiwwheivanyicovtfwineflvivcylytkelrsvtrgvkgprkvnkvfi 240
 QY 241 IIAVFICFVDFPHARIPYTLSDTRVDFDCTARNTLFPYKESLWLTSLMACLDPEIYFF 300
 DB 241 iiavficfvpfharipyltsdtrvdfdaenltfvykestlwltslnacldpfiyff 300
 QY 301 LCKSFNSLSMLKCPNSATSLSDNRKKEODGDPNEETPM 342
 DB 301 lcksfnslsmlkcpnsatslsqdnrkkegdgdpneetpm 342

RESULT 8
 AAE04385
 ID AAE04385 standard; Protein; 315 AA.
 AC AAE04385;
 XX
 DT 04-SEP-2001 (first entry)
 XX
 DE Human P2-purinegic receptor subtype, P2Y12 protein fragment.
 XX
 KW Human; P2-purinegic receptor; P2Y12; cardiac; vasotropic; thrombolytic;
 KW cerebroprotective; gynaecological; ADP; adenosine 5'-diphosphate; angina;
 KW myocardial infarction; ischemic attack; preclampsia; bleeding disorder;
 KW carotid endarterectomy; vascular graft surgery; brain disorder; migraine;
 KW peripheral vascular disease; eating disorder; depression; angioplasty;
 KW thrombocytopenic purpura; platelet aggregation; restenosis; embolism;
 KW G; disseminated intravascular coagulation; thrombosis.
 XX
 OS Homo sapiens.
 XX
 PN WO20014654-A1.
 XX
 PD 28-JUN-2001.
 XX
 PF 26-DEC-2000; 2000WO-US34998.
 XX
 PR 23-DEC-1999; 99US-0171622.
 XX
 PA (CORT-) COR THERAPEUTICS INC.
 XX
 PI Conley PB, Jantzen H, Ramakrishnan-Dubridge V, Julius DJ;
 DR Holloper G;
 DR WPI: 2001-418082/44.
 DR N-PSDB; AAD08694.
 XX

PT Novel isolated ADP receptor, termed P2Y12 receptor polypeptide, useful
 PT for identifying binding partners and for diagnostic applications
 XX
 PS Example 1: Page 84-85; 108pp; English.
 XX

CC The invention relates to ADP (adenosine 5'-diphosphate) receptor, termed
 CC as P2Y12 receptor and its corresponding cDNA molecule. P2Y12 receptor is
 CC the subtype of P2-purinegic receptor. The P2Y12 receptor is expressed
 CC selectively in the platelets and brain, and couples to a pertussis toxin-
 CC sensitive G protein (G_i). P2Y12 receptor is a G protein-coupled receptor
 CC that responds to ADP. The invention also relates to a method for
 CC identifying an agent which is useful for modulating acute myocardial
 CC infarction, unstable angina, chronic stable angina, transient ischemic
 CC attacks, strokes, peripheral vascular disease, preclampsia, deep venous
 CC thrombosis, embolism, disseminated intravascular coagulation, thrombotic
 CC thrombocytopenic purpura or a bleeding disorder, restenosis, thrombotic
 CC post CABG (coronary artery bypass graft) surgery, vascular graft surgery,

CC stent placements or insertion of endovascular devices and prostheses.
 CC P2Y12 receptor is useful for identifying binding partners and for
 CC diagnostic applications. P2Y12 receptor provides targets for screening
 CC synthetic small molecules and combinatorial or naturally occurring
 CC compound libraries to regulate platelet aggregation, vascular injury, or
 CC disease as well as schizophrenia, eating disorders, depression, migraine
 CC and other brain disorders. The present sequence is a fragment of human
 CC P2-purinergic receptor subtype, referred as P2Y12.

SQ Sequence 315 AA:

Query Match 91.9%; Score 1634; DB 22; Length 315;
 Best Local Similarity 100.0%; Pred. No. 2.6e-171;
 Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQAVNDLTSAGNLSICRDYKTOVLEPLLTVLFFVGLITNGLAMRIFQIRSKSNFI 60
 DB 1 mqavndltsagnlsicrdyktovllepllvtvllfvglltnglamrffqirsksnfi 60
 QY 61 IFLKNTVISDLMLITPFFKILSDAKLGTGPRFVCQVTSVTEFVYVYISIFGLITI 120
 DB 61 iflnkntvisdlmlitpffkilsdaklgtgprfvcqvtsvtefvyvysisifgliti 120
 QY 121 DRYQKTRPEKTSNPKNLGAKILSVIWAQWFLSLPNNMLTNRQPKNKKCSFKS 180
 DB 121 dryqktrpektspknlgakilsvisvawqwfllslpnnmltnrqpknkksfks 180
 QY 121 dtygkttrpfktsnpknlgakilsvisvawqwfllslpnnmltnrqpknkksfks 180
 QY 181 EBLGWHIEIVNYICQVIFWINEFLIVCYTLITKELYSYVTRGVGKVRKKVWYFI 240
 DB 181 eblgwhieivnyicqvifwineflivcytlitkelysyrvgvgkvrkvwkyfi 240
 QY 241 IIAVEFICFVPRFARIPYTLTSQTRDVEPCTAENTLFYVKESTLMTSLNACLDPEIYFF 300
 DB 241 iiaveficfvprrfariptytltsqtrdvepctaentlfyvkestlmtslnacldpeiyff 300
 QY 301 LCKSPFNSLISMUKC 315
 DB 301 lcksfnsismukc 315

RESULT 9

AAE04384 AAE04384 standard; Protein; 343 AA.

AC AAE04384;

DT 04-SEP-2001 (first entry)

DE Rat P2-purinergic receptor subtype, P2Y12.

KM Rat; P2-purinergic receptor; P2Y12; cardiant; vasotropic; thrombolytic;
 KM cerebroprotective; gynaecological; ADP; adenosine 5'-diphosphate; angina;
 KM myocardial infarction; ischaemic attack; preclampsia; bleeding disorder;
 KM carotid endarterectomy; vascular graft surgery; brain disorder; migraine;
 KM vascular injury; schizophrenia; eating disorder; depression; angiodysplasia;
 KM peripheral vascular disease; platelet aggregation; restenotic; embolism;
 KM thrombocytopenic purpura; stroke; pertussis toxin-sensitive G protein;
 KM GI; disseminated intravascular coagulation; thrombosis.

OS Rattus norvegicus.

PN W0200146454-A1.

PD 28-JUN-2001.

PF 26-DEC-2000; 200OWO-US34998.

PR 23-DEC-1999; 99US-0171622.

XX (COR-) COR THERAPEUTICS INC.

XX Conley PB, Jantzen H, Ramakrishnan-Dubridge V, Julius DJ;

PI Holloper G;

XX WPI; 2001-418082/44.
 DR N-PSDB; AAD08693.

PT Novel isolated ADP receptor, termed P2Y12 receptor polypeptide, useful
 for identifying binding partners and for diagnostic applications

PS Claim 14; Page 81-82; 108pp; English.

XX The invention relates to ADP (adenosine 5'-diphosphate) receptor, termed
 XX as P2Y12 receptor and its corresponding cDNA molecule. P2Y12 receptor is
 XX the subtype of P2-purinergic receptor. The P2Y12 receptor is expressed
 XX selectively in the platelets and brain, and couples to a pertussis toxin-
 XX sensitive G protein (G_i). P2Y12 receptor is a G protein-coupled receptor
 XX that responds to ADP. The invention also relates to a method for
 XX identifying an agent which is useful for modulating acute myocardial
 XX infarction, unstable angina, chronic stable angina, transient ischaemic
 XX attacks, strokes, peripheral vascular disease, preclampsia, deep venous
 XX thrombosis, embolism, disseminated intravascular coagulation, thrombotic
 XX thrombocytopenic purpura or a bleeding disorder; thrombotic and
 XX restenotic complications following angioplasty, carotid endarterectomy,
 XX post CABG (coronary artery bypass graft) surgery, vascular graft surgery,
 XX stent placements or insertion of endovascular devices and for
 XX P2Y12 receptor is useful for identifying binding partners and for
 XX diagnostic applications. P2Y12 receptor provides targets for screening
 XX synthetic small molecules and combinatorial or naturally occurring
 XX compound libraries to regulate platelet aggregation, vascular injury, or
 XX disease as well as schizophrenia, eating disorders, depression, migraine
 XX and other brain disorders. The present sequence is rat P2-purinergic
 XX receptor subtype, referred as P2Y12 receptor.

SQ Sequence 343 AA:

Query Match 86.0%; Score 1528.5; DB 22; Length 343;
 Best Local Similarity 86.9%; Pred. No. 1.2e-159;
 Matches 293; Conservative 17; Mismatches 22; Indels 5; Gaps 1;

QY 6 NLTSAPGNTSLCTRDYKTOVLEPLLTVLFFVGLITNGLAMRIFQIRSKSNFI 65
 DB 12 nltspgntslctrdyktovllepllvtvllfvglltnglamrffqirsksnfi 65
 QY 66 TVISDLMLITPFFKILSDAKLGTGPRFVCQVTSVTEFVYVYISIFGLITDRYOK 125
 DB 72 tvisdmlitpffkilsdaklgtgprfvcqvtsvtefvyvysisifglitdryok 131
 QY 126 TRPEKTSNPKNLGAKILSVIWAQWFLSLPNNMLTNRQPKNKKCSFKSEFGLV 185
 DB 132 trpfktsnpknlgakilsvisvawqwfllslpnnmltnrqpknkksfksfeglv 191
 QY 186 WHEIVNYICQVIFWINEFLIVCYTLITKELYSYVTRGVGKVRKKVWYFI 245
 DB 192 wheivnyicqvifwineflivcytlitkelysyrvgvgkvrkvwkyfi 251
 QY 246 FICQVPRFARIPYTLTSQTRDVEPCTAENTLFYVKESTLMTSLNACLDPEIYFFLCKSF 305
 DB 252 ficqvprfariptytltsqtrdvepctaentlfyvkestlmtslnacldpeiyfflcksf 311
 QY 306 RNSLISMUKCNSATSLSDNRKKEDGDPNRETPN 342
 DB 312 rnsismukcnsatslsodnrkkedgdpnretpn 343

RESULT 10

AAV94498 AAV94498 standard; protein; 387 AA.

AC AAV94498;

DT 15-SEP-2000 (first entry)

DE Rat MP-10 receptor protein.

XX G-protein coupled receptor; GPCR; MP-10 receptor; rat; CNS;
KM central nervous system; spleen; anaesthetic; analgesic.
XX
OS *Rattus* sp.
XX
PN WO200034333-A1.
XX
PD 15-JUN-2000.
XX
PF 08-DEC-1999; 99WO-SE02302.
XX
PR 10-DEC-1998; 98SE-0004274.
XX
PA (ASTRA) ASTRA PHARMA INC.
PA (ASTR) ASTRA AB.
XX
PI Ahmad S, Hoffert C, Lembo P, O'Donnell D, Walker P;
XX
XX WPI: 2000-431276/37.
DR N-PSDB; AAA48642.
XX
XX Novel G protein-coupled receptor, MP-10 receptor, useful for
PT identification of new anaesthetic and analgesic agents -
XX
PS Claim 1; Fig 2; 28pp; English.
XX
XX The present sequence is rat MP-10 receptor protein. The DNA encoding
CC this protein was identified from a rat brain stem/spinal cord cDNA
CC library. In situ hybridisation analysis showed that MP-10 receptor
CC mRNA is expressed diffusely but ubiquitously in the adult rat central
CC nervous system (CNS). The mRNA was also found in adult rat spleen.
CC MP-10 receptor protein contains several structural features
CC characteristic of a G protein coupled receptor (GPCR). MP-10
CC receptor protein is useful for identifying new anaesthetic and analgesic
CC agents. Such agents may be identified using assays designed to
CC detect agonists or antagonists capable of binding to the receptor,
XX therefore modulating intracellular signalling.
XX
XX Sequence 387 AA;

```

Query Match Similarity      84.0%: Score 1493.5; DB 21; Length 387;
Best Local Similarity      86.4%: Pred. No. 1e-15;
Matches 287; Conservative 17; Mismatches 23; Indels 5; Gaps 1.

QY      6 NLTSAAGNNTSLCTRRDKITTOVLEPPLLYLVLFEGGLTNGLAIRIPQIRSKSNFIETLKN 65
      12 | | | | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      12 nttstpgtstclscryckitcvqifpillylvifagiltteqlamrtfqlrsksnfiflkn 71

QY      66 TVYSIDLMLITLTPPEKFLISAQKGTGDLRTFCQVSVIRFYPMYISISFGLITIDRYOK 125
      72 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      72 tvysidllmlitlfpkflisdakigaghlrtlcqvcsvtytfmynsisistgiltidrylk 131

QY      126 TTRPEFTSNPKNULAKTLISYVINAEMFLSLPNMILNROPRDKNVKCKSLKEFGIV 185
      132 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      132 trtprftsspnllgakkilsvaiawfimflisipmmlttnrpkdcdtkcsflksefgiv 191

QY      186 WHEIYNYICQVWFNFELIVICYTLITRELRSVYTRGVGKVPYRKKNVNVVFITIAVF 245
      192 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      192 wheivnylcqvifwvfnflivivcyslilkelytrsvtrtgsakapkvtnkvillavf 251

QY      246 FICFVPHFHARLPVYLSQTRDVFCDTAENLTLEVYKESTLMLTSLNACIDPFIFYFLCKSF 305
      252 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      252 ficfvpfhfaripyelsqgravfcdenaenclfyvkesclwtslnacdipfiylfcksf 311

QY      306 RNSLSMLKCPNSATSLSDQNRKKKQDDGDPN 337
      | | | | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      312 rnslsmlmrlr-----stsganlkkyqgeggdps 338

```

RESULT 11
AAE04387

ID	AAE04387 standard; Protein; 267 AA.
AC	AAE04387;
XX	
DT	04-SEP-2001 (first entry)
XX	
DE	Human P2-purinergic receptor subtype, P2Y12 truncated allelic variant.
XX	
KW	Human; P2-purinergic receptor; P2Y12; cardiant; vasotropic; thrombolytic
KM	cardioprotective; gynaeological; ADP; adenosine 5'-diphosphate; angina
KM	myocardial infarction; ischaemic attack; pre-eclampsia; bleeding disorder
KM	carotid endarterectomy; vascular graft surgery; brain disorder; migraine
KM	vascular injury; schizophrenia; eating disorder; depression; angiodysplasia
KM	peripheral vascular disease; platelet aggregation; restenotic; embolism;
KM	thrombocytopaenic purpura; stroke; pertussis toxin-sensitive G protein;
KM	G1; disseminated intravascular coagulation; thrombosis; mutant; muten;
KW	variant.
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	
PN	MO200146454-AL.
XX	
PD	28-JUN-2001.
XX	
XX	
PF	26-DEC-2000; 2000WO-US34998.
PR	23-DEC-1999; 99US-0171622.
XX	
PA	(CORT-) COR THERAPEUTICS INC.
XX	
PI	Conley PB, Jantzen H, Ramakrishnan-Dubridge V, Julius DJ;
XX	Hollopeter G;
DR	WPI; 2001-418082/44.
XX	N-PSDB; AAD08700.
XX	
PT	Novel isolated ADP receptor, termed P2Y12 receptor polypeptide, useful
XX	for identifying binding partners and for diagnostic applications -
PS	Claim 29; Page 91-92; 10pp; English.
XX	
XX	
CC	The invention relates to ADP (adenosine 5'-diphosphate) receptor, termed
CC	as P2Y12 receptor and its corresponding cDNA molecule. P2Y12 receptor is
CC	the subtype of P2-purinergic receptor. The P2Y12 receptor is expressed
CC	selectively in the platelets and brain, and couples to a pertussis toxin
CC	sensitive G protein (G _i). P2Y12 receptor is a G protein-coupled receptor
CC	that responds to ADP. The invention also relates to a method for
CC	identifying an agent which is useful for modulating acute myocardial
CC	infarction, unstable angina, chronic stable angina, transient ischaemic
CC	attacks, strokes, peripheral vascular disease, pre-eclampsia, deep venous
CC	thrombocytopaenic purpura or a bleeding disorder; thrombotic and
CC	restenotic complications following angioplasty, carotid endarterectomy,
CC	post CABG (coronary artery bypass graft) surgery, vascular graft surgery,
CC	stent placements or insertion for endovascular devices and prostheses.
CC	P2Y12 receptor is useful for identifying binding partners and for
CC	diagnostic applications. P2Y12 receptor provides targets for screening
CC	synthetic small molecules and combinatorial or naturally occurring
CC	compound libraries to regulate platelet aggregation, vascular injury, or
CC	disease as well as schizophrenia, eating disorders, depression, migraine
CC	and other brain disorders. The present sequence is human P2-purinergic
CC	receptor subtype, P2Y12 truncated allelic variant. The variant is
CC	obtained by deleting two bases 'CA' from position 789-790 of the wildtype
CC	human P2Y12 receptor cDNA, resulting in amino acid changes from position
XX	240 of the wildtype human P2Y12 receptor.
XX	
Sequence	267 AA.

Query Match	69.6%;	Score 1237.5;	DB 22;	Length 267;
Best Local Similarity	95.7%;	Pred. No. 9.4e-128;		
Matches 242;	Conservative	3;	Mismatches 7;	Indels 1;
				Gaps 1

FT	Domain	/label= Transmembrane_domain_(27m)
FT		83..96
FT		/label= Extracellular_domain
FT		/note= "First EC loop"
FT	Domain	97..118
FT		/label= Transmembrane_domain_(37m)
FT		119..135
FT	Domain	/label= Intracellular_domain
FT		/note= "Second IC loop"
FT		136..160
FT	Domain	/label= Transmembrane_domain_(47m)
FT		161..188
FT	Domain	/label= Extracellular_domain
FT		/note= "Second EC loop"
FT		189..211
FT	Domain	/label= Transmembrane_domain_(57m)
FT		212..231
FT	Domain	/label= Intracellular_domain
FT		/note= "Third IC loop"
FT		232..252
FT	Domain	/label= Transmembrane_domain_(67m)
FT		253..280
FT	Domain	/label= Extracellular_domain
FT		/note= "Third EC loop"
FT		281..300
FT	Domain	/label= Transmembrane_domain_(77m)
XX		
PN		WO200131014-A2.
XX		
PD		03-MAY-2001.
XX		
PF		27-OCT-2000; 2000WO-US29601.
XX		
PR		27-OCT-1999; 99US-0427653.
PR		27-OCT-1999; 99US-0427859.
PR		27-OCT-1999; 99US-0428020.
PR		27-OCT-1999; 99US-0428114.
PR		28-OCT-1999; 99US-0428517.
PR		28-OCT-1999; 99US-0428555.
PR		28-OCT-1999; 99US-0428676.
PR		28-OCT-1999; 99US-0429695.
PR		03-DEC-1999; 99US-0454399.
PR		12-JAN-2000; 2000US-0481794.
XX		
PA		(PHMA) PHARMACIA & UPJOHN CO.
XX		
PI		Vogeli G, Wood LS, Merchant K;
XX		
DR		WPI: 2001-328653/34.
DR		N-PSDB; AAD06503.
XX		
PT		Seven transmembrane receptor polypeptides and polynucleotides, useful
PT		for treating neurological or psychiatric disorders, e.g. schizophrenia,
PT		as well as for identifying compounds useful for treating schizophrenia
PT		-
XX		
PS		Claim 1; Page 10-11; 215pp; English.
XX		
CC		The invention relates to human G protein-coupled receptor (GPCR) and
CC		their corresponding DNA molecules. GPCR is also referred as seven
CC		transmembrane receptor. G protein-coupled receptor protein is useful for
CC		treating neurological disorder, particularly schizophrenia. GPCR protein
CC		is also useful for identifying compounds useful for treating
CC		schizophrenia. These compounds are also useful for treating other
CC		neurological and psychiatric diseases, e.g. depression, anxiety, bipolar
CC		disease, affective disorders, attention deficit hyperactivity disorder/
CC		attention deficit disorder, epilepsy, neuritis, neuroschizophrenia, neuropathy,
CC		neurosis, Alzheimer's disease, Parkinson's disease, migraine and senile
CC		dementia. The invention also provides genetic screening procedures that
CC		entail analysing a person's genome with respect to GPCR. The vectors are
CC		useful for the recombinant production of the GPCR's. The present sequence
CC		is human CON203 G protein-coupled receptor (GPCR) protein.
XX		

Sequence	333 AA:
Query Match	46.5%; Score 827; DB 22; Length 333;
Best Local Similarity	48.7%; Pred. No. 1,9e-82;
Matches 154; Conservative	57; Mismatches 103; Indels 2; Gaps 1;
Db	
Qy	17 CTRDYKTRQVLFPLLYTVLFFVGLITNGLAMRIFFOIRKSNFIIFLKNVTYISDLMLIT 76
Dd	15 pcdrtirglvfpalytvlvfltgllntlaifvfhlpssstfilylknltvaadlmtlm 74
Qy	77 FPFKLISPAKLGTLGRFVQCVSVIRFYFTYISISPLGLTTIDRYQKTTPEPFTSNK 136
Dd	75 lpfkliscdshlapwglrafcvrfcstsvlfyctmyglvllglaiafarklilpplnlfik 134
Qy	137 NILGKIISVYIWMFNLPLNMLITLRNOPDKNVKCSFLKSEGLWHEIVYVICOV 196
Dd	135 kpvfakrtvsilfwlilvflislpnmlllnkbeatpsvkkcaaslkpqlglkwbgumvnlcgf 194
Qy	197 IFWINEFLIVICYTLITKELVRSYVTRGVGKVPKKVNVKVIILIAVEFLICVDFEHPH 256
Dd	195 ifwgfllimlflvyvialkkyvdgsyyskkskdknnkkllegkfvvavavfvcfapfhfar 254
Qy	257 IPRYISQRRDVFDCIAENLTFYKSESTLMYLSLNACLDPFIFFFLCKSRNLSLMKCP 316
Dd	255 vpythsqcnnkdkcdclqnlqflakakettflaactnclompllyifllokkftekllpcmq--g 312
Qy	317 NSATSLSDNNRKEOD 332
Dd	313 rktassqgnhsqcd 328

Search completed: September 6, 2002, 15:30:19
Job time: 148 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 6, 2002, 15:28:52 ; Search time 17.7 Seconds
(without alignments)
1856.641 Million cell updates/sec

Title: US-09-827-937a-2

Perfect score: 1778

Sequence: 1 MQAVDNLTSAPGNTSLCTRD.....SQDNRRKKEDGGDPNETPM 342

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR-71:.*
1: pirl:.*
2: pirl:.*
3: pirl:.*
4: pirl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	394	22.2	342	2 A40191	platelet-activatin
2	392.5	22.1	342	2 S13658	platelet-activatin
3	379.5	21.3	361	2 B45680	G protein-coupled
4	366	20.6	341	2 S63666	platelet-activatin
5	362	20.4	341	2 S43252	platelet-activatin
6	357.5	20.1	308	2 I50241	G protein-coupled
7	339	19.1	359	2 S15403	angiotensin II rec
8	330	19.0	344	2 T09508	intron 17 putinerg
9	329	18.5	359	2 I39418	angiotensin II rec
10	326	18.3	359	2 S44425	angiotensin II rec
11	325.5	18.3	359	2 I48705	protenase activat
12	325	18.3	359	2 A48857	angiotensin II rec
13	321	18.1	359	2 JC1104	angiotensin II rec
14	321	18.1	370	2 JC5549	heptahelical P215-
15	319	17.9	359	2 A42656	angiotensin II rec
16	318	17.9	359	2 JC2134	angiotensin II rec
17	318	17.9	359	2 JC1194	angiotensin II rec
18	318	17.9	359	2 JH0621	angiotensin II rec
19	317.5	17.9	365	2 S68208	G protein-coupled
20	317.5	17.9	368	2 I56517	mu opioid receptor
21	314.5	17.7	398	2 I56504	mu opioid receptor
22	314	17.7	359	2 J01516	angiotensin II rec
23	313.5	17.6	380	2 I38435	angiotensin recept
24	310.5	17.5	362	2 JN0654	angiotensin II rec
25	309	17.4	392	2 S65633	opioid receptor mu
26	309	17.4	400	2 I56553	mu opiate receptor
27	306	17.2	397	2 S66518	protenase-activat
28	304.5	17.1	398	2 A57510	mu opioid receptor
29	299	16.8	380	2 JC2434	kappa opioid recep

30	298.5	16.8	365	2 S68679	G protein-coupled
31	298	16.8	380	2 A48227	kappa opioid recep
32	297.5	16.7	359	2 I51372	angiotensin II rec
33	297.5	16.7	360	2 A53611	interleukin-8 rece
34	297	16.7	380	2 A55259	kappa opioid recep
35	296.5	16.7	420	2 I51667	thrombin receptor
36	296	16.6	380	2 S36143	kappa opioid recep
37	295	16.6	380	2 JC2338	kappa opioid recep
38	292.5	16.5	362	2 S33733	G protein-coupled
39	291.5	16.4	373	2 A47556	ATP receptor P2u -
40	290.5	16.3	352	2 A45747	neuropeptide Y/pep
41	284.5	16.0	333	2 I38974	G protein-coupled
42	282.5	15.9	352	2 G00048	fusin (LESTRA) - c
43	282	15.9	352	2 A43113	chemokine (C-C) re
44	282	15.9	355	2 J01231	interleukin-8 rece
45	281.5	15.8	353	2 S28787	neuropeptide Y/pep

ALIGNMENTS

RESULT 1
A40191
platelet-activating factor receptor - human
C:Species: Homo sapiens (man)
C:Date: 28-Aug-1992 #sequence, revision 28-Aug-1992 #extl, change 20-Jun-2000
C:Accession: A40191; JH0479; A41079; JC1359; A42831; I51923
R:Kunz, D.; Gerard, N.P.; Gerard, C.
J. Biol. Chem. 267, 9101-9106, 1992
A:Title: The human leukocyte platelet-activating factor receptor, cDNA cloning, cell
A:Reference number: A40191; MUID:92250505
A:Accession: A40191
A:Molecule type: mRNA
A:Residues: 1-342 <KUN>
A:Cross-references: GB:M6674; NID:9456293; PIDN:AAA60002.1; PID:9456294
R:Ye, R.D.; Prossnitz, E.R.; Zou, A.; Cochrane, C.G.
Biochem. Biophys. Res. Commun. 180, 105-111, 1991
A:Title: Characterization of a human cDNA that encodes a functional receptor for plat
A:Reference number: JH0479; MUID:92028922
A:Accession: JH0479
A:Molecule type: mRNA
A:Residues: 1-342 <YE>
A:Cross-references: GB:M80436; NID:9189537; PIDN:AAA60001.1; PID:9189538
A:Experimental source: GB:granulocyte, cell line HL-60 all
R:Nakamura, M.; Honda, Z.; Izumi, T.; Sekanaka, C.; Mutoh, H.; Minami, M.; Bito, H.;
J. Biol. Chem. 266, 20400-20405, 1991
A:Title: Molecular cloning and expression of platelet-activating factor receptor from
A:Reference number: A41079; MUID:92041873
A:Accession: A41079
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-342 <NAK>
A:Cross-references: GB:DI0202; GB:D90433; NID:9219975; PIDN:BAA01050.1; PID:9219976
R:Sugimoto, T.; Tsuchimochi, H.; McCreight, C.G.A.; Mutoh, H.; Shimizu, T.; Kurachi, Y
Biochem. Biophys. Res. Commun. 189, 617-624, 1992
A:Title: Molecular cloning and characterization of the platelet-activating factor rec
A:Reference number: JC1359; MUID:93112021
A:Accession: JC1359
A:Molecule type: mRNA
A:Residues: 1-315, 'N', 317-342 <SUG>
A:Experimental source: heart
A>Note: the authors translated the codon AAT for residue 316 as Lys
R:Sejiried, C.E.; Schweickart, V.L.; Godiška, R.; Gray, P.W.
Genomics 13, 833-834, 1992
A:Title: The human platelet-activating factor receptor gene (PTAFR) contains no intro
A:Accession: A42831; MUID:92347886
A:Molecule type: DNA
A:Residues: 1-226, 'TG', 229-342 <SEY>
A:Cross-references: GB:M88177; NID:9190697; PIDN:AAA60214.1; PID:9190698
A>Note: sequence extracted from NCBI backbone (NCBIN:109813, NCBIIP:109814)
R:Chase, P.B.; Halonen, M.; Regan, J.W.
Am. J. Respir. Cell Mol. Biol. 8, 240-244, 1993

A:Title: Cloning of a human platelet-activating factor receptor gene: evidence for an 11
A:Reference number: I51923; MUID:93192035
A:Accession: I51923
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-342 <RES>
A:Cross-References: GB:S56396; NID:g298580; PIDN:AA625755.1; PID:g298581
C:Genetics:
A:Gene: GDB:PTAFR
A:Cross-References: GDB:128806; OMIM:173393
A:Map position: 1p35-1p34.3
C:Superfamily: ATP receptor P2u
C:Keywords: G protein-coupled receptor; transmembrane protein
F:17-38/Domain: transmembrane #status predicted <TRI>
F:54-75/Domain: transmembrane #status predicted <TRI>
F:92-113/Domain: transmembrane #status predicted <TRV>
F:134-155/Domain: transmembrane #status predicted <TRV>
F:184-205/Domain: transmembrane #status predicted <TRV>
F:233-253/Domain: transmembrane #status predicted <TVI>
F:277-297/Domain: transmembrane #status predicted <VII>

Query Match	22.2%	Score 394	DB 2	Length 342
Best Local Similarity	32.6%	Pred. No. 1.6e-26		
Matches 107; Conservative	61	Mismatches 134	Indels 26	Gaps 10

```

0Y 11 PGNTEJCRDKKICQVPELLLYLTVLFPVGLTDLARIFEQIR--SKSNFI-IPLKNV 67
Db 3 PHDSSHMOSEERYT--LEPIYYSITIFVLGIVANKVYLVAMVARLPCCKKFEIKIEMVNL 60
0Y 68 ISDLMLITTEPPKILSDAKLTGCPRLRFVCOVYSVITYETMYSISLGLITDRQKTT 127
Db 61 MADMFLTELLTPMLVYYOONMILLPKFLCVACCLFEIINTYCSVALGIVTYNRQOAVT 120
0Y 128 RPEKTSNERNLGAKILSVIVM----AFMELSLPMILITNRPDRK--NNKCSFLK 179
Db 121 RPIKTAQANTRRKRGISLSLVIVMAIVGASVFLIDS---TNVPPDASGANTRC-FEH 176
0Y 180 SEFGLYMHEIYNYICQVEMFNFLVLYCYLLITLKELYRSTVYTRGKGYKPKKRVANKYF 239
Db 177 YEKGSVPVLLIHIHIVSEFVLPFLITLFCNLVLIIRTLMPVOOQRNAEYKRRALMM-VG 235
0Y 240 IIAVFFICFVPFHFARIPRYLTISOTRBDVFCDTAENLTFFYKESHTLWTSINACLDPEIF 299
Db 236 TVLAVFITICFVPHVYUQDPLTAEEL-GRQDSKFRQALINDAHQVTLGLSTNCVLDPEYIC 294
0Y 300 FLCKSFNR-----SLISMLCNSKAT 320
Db 295 FLTKFRRKHLTEKEYSMRSSKRCGRAT 322

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RESULT 2
S13638
platelet-activating factor receptor - guinea pig
C:Species: Cavia porcellus (guinea pig)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 08-Oct-1999
C:Accession: S13638
R:Honda, Z.; Nakamura, M.; Miki, I.; Minami, M.; Watanabe, T.; Seyama, Y.; Okado, H.; T
Nature 349, 342-346, 1991
A:Title: Cloning by functional expression of platelet-activating factor receptor from gu
A:Reference number: S13638; M01D:J1101726
A:Accession: S13638
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-342 <HON>
A:Cross-references: GB:X56736; NID:g49442; PIDN:CAA0060.1; PID:g49443
A>Note: the species of guinea pig is not identified; in Genbank entry CCPAFREC, release
A:Superfamily: ATP receptor P2u

	Score	DB 2, Pred. No. 2.1e-26;	Length 342;	
Query Match	22.1%;			
Best Local Similarity	30.7%;			
Matches 103; Conservative	66;	Mismatches 146;	Indels 21;	Gaps 9;

[illegible]

RESULT 3
B45680
G protein-coupled peptide receptor ERI 2 - human
C:Species: Homo sapiens (man)
C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C:Accession: B45680
R:Birkenbach, M.; Josefsen, K.; Yalamanchilli, R.; Lenoir, G.; Kieff, E.
J. Virol. 67, 2209-2220, 1993
A:Title: Epstein-Barr virus-induced genes: first lymphocyte-specific G protein-couple
A:Reference number: A45680, M0ID:9318173
A:Accession: B45680
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-361 <BIR>
A:Cross-references: GB:I08177; NID:Q292056; PIDN:AAA5924.1; PID:9292057
A:Experimental source: B:Lymphocytes
A:Note: sequence extracted from NCBI backbone (NCBIN:127096, NCBIR:127097)
C:Superfamily: ATP receptor P2u
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match	21.3%	Score 379.5	DB 2	Length 361
Best Local Similarity	26.0%	Pred. No. 3e-25		
Matches 94	Conservative 84	Mismatches 152	Indels 31	Gaps 11

```

0Y 1 MOAVDNLT-----SAPKNSLCTRDYKITOVYFLLYLVFVGGLITGLAMRIEFOJRSK 56
Db 3 IOMANNETPSGATPOGNCDDIAHSHSTARIVLPMPLHLSVFIIGVLGNLLVLYVQRRK 62
0Y 57 SN-FIIEKNTVISDLMLITFEFKIL-----SDAKGTGRLREYCOVSVIETFYMYI 110
Db 63 INSTLLSVNLVIDILFTTALPRIVAYMGFEWRRGDA-----LCRITALFYINTYA 117
0Y 111 SISFLGLITDRYOKTRTPEKTSNPKULLGAKILSVIYAMFLLSLPNMI--L7NRQPR 168
Db 118 GVNEMTCLSIDREFLAVVHPRLRYNKRIRIEHAKGVCIFWMLIVPQOLPRLINPMSKOAE 177
0Y 169 DKVAKCSEFLSESGIWMHELVNIGOVIMINFLIYVCYTLITREKLS-----YVRT 223
Db 178 RITCEYRNEFETKSLRP--LLGACFIVGLPLITILICISQICCKLFPTAKQNPLETE 235
0Y 224 RGVGVKPEKKVNVVFIILIAFFCIEFPFHARIPYLSQTR--DYEDCAENMTLFYVKE 281
Db 236 SGVKN---KALNT--LIIILIVFVCLFPHYHAIQHHIKRLRSNPLFECGORSFOLSH 291
0Y 282 STWMTSLNACLDPFIYFELCKSRNLSLMKCPNSATLSLSDNNRKKEDGSDPNEETP 341

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Db 292 FTVCUAMNCCMPFIYFACKGKRYKVMK-LK-RQYVSLSISSAVKSAPEENSEMETEQ 350

Qy 342 M 342

Db 351 M 351

RESULT 4

S6366

platelet activating factor receptor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000

C:Accession: S63666

R:Shi1, S.; Matsuda, Y.; Nakamura, M.; Waga, I.; Kume, K.; Izumi, T.; Shimizu, T.

Biochem. J. 314, 671-678, 1996

A:Title: A murine platelet-activating factor receptor gene: cloning, chromosomal localization

A:Reference number: S63666; MUID:96239129

A:Accession: S63666

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-341 <ISH>

A:Cross-references: EMBL:D50872; NID:91256924; PIDN:BAA09468.1; PID:91256925

C:Superfamily: ATP receptor P2u

Query Match 20.6%; Score 366; DB 2; Length 341;

Best Local Similarity 29.9%; Pred. No. 4, 1e-24;

Matches 96; Conservative 64; Mismatches 133; Indels 28; Gaps 10;

Qy 20 DYKIQVLPPLTYVLPFVGLITNGLAMRIEFOI--RSKSNFI-IFLKNYISDLMLIT 76

10 DSEFRYTLFPYIVSYIFILGVANGYVLMVFANLYPSKRLNEIKIFMVLTMADLLFLIT 69

Qy 77 FPKILSDAKLGTPLRFCQVTSVIFETMYISIFLGLITIDRYOKTRPFTSNPK 136

70 LPLMIYVYNSNEGDWILPFLCNVACLEFINTYCSVAFLGVITNNKYLQAVAPIKTAQAT 129

Db 137 NLGAKISVIVAFM-----FLSLPMLITNROPDKNVKCSFLKSEFG--LYWHE 188

130 TRKRGISLTIWIVATASFLATDSNLYPNKDGSGNITRCHEHPYSPVLIVAV 189

Qy 189 IVNYICQVIFWIMFLI-VIVCYTLTKELYSVTRGVCKVPRKKNVAVPIIAVFI 247

190 FIACGEFLVFILFYCNILVIITLLQPMROO--RKAGV----KRALMVCOTVLAVFI 243

Qy 248 CVPPFPAIPIPTLSQTRVDCTAENTLEFYKESFLMTLSNACDPIYFLCKSPFN 307

244 CVPFHVQVLPMTLAEIG--YQTFHQAIINDAHQITLLCLSTNCVLDPIYICFLTKKPK 301

Qy 308 -----SLISMLKCPNSATS 321

302 HLESEKYSMRSSKRC-SRATS 321

RESULT 5

S43252

platelet-activating factor receptor - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 24-Nov-1999

C:Accession: S43252

R:Blito, H.; Honda, Z.; Nakamura, M.; Shimizu, T.

Eur. J. Biochem. 221, 211-218, 1994

A:Title: Cloning, expression and tissue distribution of rat platelet-activating-factor-

A:Reference number: S43252; MUID:94222063

A:Accession: S43252

A:Molecule type: mRNA

A:Residues: 1-341 <RNT>

A:Cross-references: GB:004740; NID:9470384; PIDN:AAA18422.1; PID:9470385

C:Superfamily: ATP receptor P2u

Query Match 20.4%; Score 362; DB 2; Length 341;

Best Local Similarity 28.9%; Pred. No. 9e-24;

Matches 96; Conservative 66; Mismatches 120; Indels 50; Gaps 10;

Qy 20 DYKIQVLPPLTYVLPFVGLITNGLAMRIEFOI--RSKSNFI-IFLKNYISDLMLIT 76

10 DSEFRYTLFPYIVSYIFILGVANGYVLMVFANLYPSKRLNEIKIFMVLTMADLLFLIT 69

Qy 77 FPKILSDAKLGTPLRFCQVTSVIFETMYISIFLGLITIDRYOKTRPFTSNPK 136

70 LPLMIYVYNSNEGDWILPFLCNVACLEFINTYCSVAFLGVITNNKYLQAVAPIKTAQAT 129

Qy 137 NLGAKISVIVAFM-----FLSLPMLITNROPDKNVKCSFLKSEFG--LYWHE 188

130 TRKRGISLTIWIVATASFLATDSNLYPNKDGSGNITRCHEHPYSPVLIVAV 189

Qy 177 FLKSEFGLVMEIYNYICQVIFWIMFLI-VIVCYTLTKELYSVTRGVCKVPRKKNV 236

190 FITSCFLVIF-----LFYCNMVIIT--HLLTRP-----VROQRKPEVRBALMM 233

Qy 237 KVFIIIAVFICFVPEHFAPIPTLSQTRVDCTAENTLEFYKESFLMTLSNACDPI 296

234 -VCTVLAIVFICFVPHVQVLPMTLAEIG--YQTFHQAIINDAHQITLLCLSTNCVLDPI 290

Qy 297 IYFELCKSPFN-----SLISMLKCPNSATS 321

291 IYFELCKSPFN-----SLISMLKCPNSATS 321

RESULT 6

150241

G protein-coupled receptor 6H1 - chicken

N:Alternate names: purinoceptor 6H1

C:Species: Gallus gallus (chicken)

C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 02-Jun-2000

C:Accession: I50241; JC4618

R:Kaplan, M.H.; Smith, D.I.; Sundick, R.S.

J. Immunol. 151, 628-636, 1993

A:Title: Identification of a G protein coupled receptor induced in activated T cells.

A:Reference number: I50241; MUID:93329058

A:Accession: I50241

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-308 <KAP>

A:Cross-references: GB:I06109; NID:9304383; PIDN:AAB06587.1; PID:9304384

R:Webb, T.E.; Kaplan, M.G.; Barnard, E.A.

Biochem. Biophys. Res. Commun. 219, 105-110, 1996

A:Title: Identification of 6H1 as a P2z purinoceptor. P2Y5.

A:Reference number: JC4618; MUID:96190677

A:Accession: JC4618

A:Molecule type: mRNA

A:Residues: 1-308 <WEB>

A:Cross-references: GB:L06109; NID:9304383; PIDN:AAB06587.1; PID:9304384

A:Experimental source: T-cells

C:Comment: This receptor plays a role in T-cell activation.

C:Genetics:

A:Gene: P2Y5

C:Superfamily: ATP receptor P2u

C:Keywords: G protein coupled receptor; transmembrane protein

F:15-40/Domain: transmembrane #status predicted <TM1>

F:51-74/Domain: transmembrane #status predicted <TM2>

F:89-109/Domain: transmembrane #status predicted <TM3>

F:133-153/Domain: transmembrane #status predicted <TM4>

F:177-201/Domain: transmembrane #status predicted <TM5>

F:227-248/Domain: transmembrane #status predicted <TM6>

F:269-292/Domain: transmembrane #status predicted <TM7>

Query Match 20.1%; Score 357.5; DB 2; Length 308;

Best Local Similarity 29.5%; Pred. No. 2e-23;

Matches 87; Conservative 68; Mismatches 125; Indels 15; Gaps 8;

Qy 14 TSLCTRYKITYVLPPLTYVLPFVGLITNGLAMRIEFOI--RSKSNFI-IFLKNYISDLMLIT 72

3 SSNCSTEDSEKRYLYLGVCFVSMVFVGLIANCVAIYIFTLTKVKNETTYTLMALISDL 62

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0Y 73 MLPEPFIISDAGKIGBELTFFQCVATSVIEFTWTMISISFGLITIDRQKTTREPKT 132
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 63 FVFILPEFIITYFV--VRNPFEDVDKCTISVLEFYNNMGSIILFELICISVDREFLAVHPERS 121
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
0Y 133 SNPKNLGAKILSVYVAFMFLSLPLPMNII--TNRQPRDKNVKCC--SPKSEFGIWNHE 188
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 122 KTLRFRKRRARIVCAVAVMTTLAGSTPASFPQSTNRQ--NNTBQRCFENPESTWKYYLSR 180
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
0Y 189 IVNIVICQVIFINFLIYIVCTLTITKELYSRYNTRGVGKVRPKVNVKFIIVAFETC 248
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 181 IVIFLEIYGFPIPIILANTGCTSWLRLNKLPLTSLR--NKLTSKKVYLMKFIHVLHYFCFC 238
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
0Y 249 FVPEHFARIPYLTQSOTRDVECC--TADNLTIFYKRETIWLTSLNACLDPIYTFE 300
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 239 FVPIPNITILIKSLMRQTQWIMCSVYVIAVRIMYAPV--TLCIIVASNCCFDIVYFE 290
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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RESULT 7
S15403
angiotensin II receptor type 1 - bovine
C:Species: Bos primigenius indicus x Bos primigenius taurus (cattle)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Nov-1996
R:Accession: S15403
R:Sasaki, K.; Yamano, Y.; Bardhan, S.; Iwai, N.; Murray, J.J.; Hasegawa, M.; Matsuda, Y.
Nature 351, 230-233, 1991
A>Title: Cloning and expression of a complementary DNA encoding a bovine adrenal angiotensin
A:Reference number: S15403; MUID:S1251900
A:Accession: S15403
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-359 <SAS>
A:Cross-references: GB:X62294; NID:g43; PID:CAA44182.1; PID:g44
C:superfamily: vertebrate rhodopsin

Query Match	19.1%	Score 339	DB 2	Length 359
Best Local Similarity	27.9%	Pred. No. 9.2e-22		
Matches	95	Conservative	62	Mismatches 143; Indels 40; Gaps 10;
Qy	26	VLEPLLYLVLFVVGILITNGL-AMRIEFOIQRKSNFIIFLKNVIVISDLMLITLFFPKRIISD	84	
Db	29	IMIFPLYSIIIFVVGLEFGNSLVVIVYIFPFKLTQVSAVELMLALDLCFLITPLMAVYT	88	
Qy	85	AKLGTGPLETFCQVTSVYIEFTMYISISFGLITIDRYOKTTRPQSNPKNLGAKIL	144	
Db	89	AMEYKMPGNYLCKITASASVSENLASAVELLTCLSIDRYALIVHMKSRSLRRTMLVAVYT	148	
Qy	145	SVVIAFAFELLSLPMILITN-RQPRDKVVKCSF-----LKSEFGLVHEIYNYTCQ	195	
Db	149	CIITMLGLASLPITIIHRNVEFIENTNITQCAFYESONSTLPLVGLGLT-KNIGLFL--	205	
Qy	196	VIFWFIPLIVAYCYLLIRKLEYRSYVRTRGVGKVRKVNKVFIIIAVFICFPRFHEA	255	
Db	206	---FPFLIITLSTLIMKLTAKAEIOLK---MKPRKDIKRIIALVALVFPF-----FS	252	
Qy	256	RIPPTLSQTRVYF-----DCTAENTLFYVKESTLMLTSLNACIDPEIYFELCKSFNS	308	
Db	253	WVPHQIFEMFQVLLIOLGLIRDCKEIDIVDTAMPITICLAYFNQNCINPLFYFGLKKFKKY	312	
Qy	309	LISMUK-CPNSATSLSQDNRK-----KEQDGGPNEETP	341	
Db	313	FLQILKTIYPPKAKSHSNLSTMASTLSTYRPSNGNSSTKKP	352	

RESULT 8
T09508
intron 17 putative receptor p2v5 - human
N:Alternate names: G-protein coupled receptor
C:Species: Homo sapiens (man)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 24-Nov-1999
C:Accession: T09508
R:Bohm, S.K.; Trump, A.; Khltin, L.M.; Kong, W.; Payan, D.G.; Bunnett, N.W.

A:Submitted to the EMBL Data Library, April 1997
A:Description: The human purinergic receptor P2U5 is encoded in intron 17 of the retA
A:Reference number: Z16705
A:Accession: 109508
A:Status: preliminary; translated from GR/EMBL/DBD
A:Molecule type: mRNA
A:Residues: 1-344 <BOH>
A:Cross-references: EMBL:AF000546; NID:z2232068; PID:g2323069
C:Genetics:
A:Map position: 13
C:Superfamily: ATP receptor P2U
C:Keywords: G protein-coupled receptor; transmembrane protein

[illegible]

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RESULT      9
139418
angiotensin II receptor type 1b - human
C:Species: Homo sapiens (man)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 24-Nov-1999
R:Accession: I39418
R:Kuroda, S
Biochem. Biophys. Res. Commun. 199, 467-474, 1994
A:Title: Novel subtype of human angiotensin II type 1 receptor: cDNA cloning and expr
A:Reference number: I39418, MUID:94183213
A:Accession: I39418
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-359 <RES>
A:Cross-references: GB:J3814, NID:g471120, PIDN:BAA02968.1, PID:g471121
C:Superfamily: vertebrate rhodopsin

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[illegible]

[illegible][illegible]

A:Title: The mouse proteinase-activated receptor-2 cDNA and gene. Molecular cloning a
A:Reference number: 148705; MUID:95197620
A:Accession: 148705
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-399 <RES>
A:Cross-references: EMBL:Z48043; NID:9663020; PIDD:CMAB88097.1; PID:9663021
C:Superfamily: ATP receptor P2u

Query Match	18.3%	Score 325.5	DB 2	Length 399
Best Local Similarity	27.6%	Pred. No. 1.5e-20		
Matches	92	Conservative	73	Mismatches 141; Indels 27; Gaps 12
QY	22	KITQVLFPLLVLFVEFGHITNGLAMRIE-FQIRSKSNFIPLKNTVSDILMLITFPER	80	
DB	74	KLTTFELRPVYIIVEIVIGISNGMALMIFELFTKKKHRAVIYIMANLADLSVIMFLK	133	
QY	81	ILSDAKLGTGLRTVCOVTSVIEFTYMWIISISPLGLTIDRYQKTRTPEKTSNPNLGL	140	
DB	134	ISYHLGNMVMYGEALCKVLLIGFFPGNMKCSILTFMTCSLVQRYWYIVNPM-GHPRKKAN	191	
QY	141	AKI-LSVYIMANFMIPLSPNML--TNQPRKKNVKKCSFLKSEFGIYVHELVNTICQV-	196	
DB	132	IANGVSLAIWMLIFVTTPIPLVMKOTIYIRA-LNTTCHDVLPEEVLV-GDMFNFLSLA	249	
QY	197	--IFWINEFLIVVCYTLITLTKELRSYSVTRGCVKPRKVNKVFILIAVFICVPPHF	254	
DB	250	IGVFELPALLTASAVVIMIKTLRSSAMDEHSKK--RQAKILILITVLAMYTICAPSML	307	
QY	255	AR-IPYTLISQTRDVEDCAENTLEFYVKESTLMTLSLNACLDFIYFPLCKSFRNSLSML	313	
DB	308	LLVHYVFLIKTO-----RQSHVVALYLVALCLSTLNSCIDPFVYVYFVSKDFRDHARNL	361	
QY	314	KCPNSAT-----SLSDGNRRKKEGGGDPNEET	340	
DB	362	LGRSVRTVNRMOISLS-SNKRFSRKSGLSVSSST	393	

```

RESULT      12
A48857      angiotensin II receptor type I - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999
C:Accession: A48857
R:Burns, K.D.; Inagami, T.; Harris, R.C.
A>Title: Cloning of a rabbit kidney cortex AT1 angiotensin II receptor that is presen
A:Reference number: A48857; MUID:93236091
A:Accession: A48857
A>Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-359 <BUR>
A:Cross-references: GB:S59041; NID:g299614; PIDN:AAB26239.1; PID:g299615
A:Experimental source: proximal tubule cells
A>Note: sequence extracted from NCBI backbone (NCBIN:129600, NCBIP:129601)
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match          18.3%; Score 325; DB 2; Length 359;
Best local similarity 29.2%; Pred. No. 1.se=20;
Matches 92; Conservative 55; Mismatches 146; Indels 22; Gaps 8;

QY      26 VLFLPLVLFVFGLITNGLA-MRIFFOIRKSNFIIFLKRTVTSIDLMLITPEPKILSD 84
       |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB      29 VMPLVLIIIVGAIIFGSLAVIIVFYFMKLTVASVFLNLALADLCFLTLTLPMAVYT 88

QY      85 AKLTGPLRTFVCQVSIVIFYFTWVISISFLGITIDRYOKTRTPFKTSNPNKLLGAKIL 144
       |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB      89 AMERWRPFGNVLCLIASASVSFNLTASVFLTCLSIDRYLAIIVPMKSRLRRITLVAKVT 148

QY      145 SVVIAMFELLISDPMILITN-RQPRDKNVKKCSF-----LKSEGLVNHETIVNTQ 195

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Db      149 CIIIMLAGLASPAIIRHNFFIENNTITVCAFYHESONSTLPGLGLT-KNIIIGFL-- 205
      196 VIFWINEFLIVCYTLITTELKELYSVTRGVKVRKKVKNKVF-IIAVEFICVPEHF 254
      206 ----FPFLIITSLTILMKALKKAVEIOK---NKPRNDIDFKIIMAVLFFEFSSVPHQI 258
QY      255 ARIPYTLISQTRDVFPCYAEENLFLVYKESTLMLTSLNACLDPEIFPEFLCKSPFNLSIMLK 314
Db      259 FTFLIDVLIQGLGVHDCRIADIVDTAMPITICIAVFNCLNPLFGFLGKKRKYFLQLLK 318
QY      315 -CPNSATSLSDNRK 328
Db      319 YIRPKAKSHSNLSTK 333

RESULT 13
JC1104
Angiotensin II receptor type 1 - human
N:Alternate names: angiotensin II receptor 1A
C:Species: Homo sapiens (man)
C:Date: 09-Oct-1992 #sequence, revision 09-Oct-1992 #text, change 21-Jul-2000
C:Accession: J01104; J01402; JH0574; JH0267; A44014; S18983
R:Maizy, C.A.; Hwang, O.; Eglit, A.M.; Wu, L.H.; Chung, F.Z.
Biochem. Biophys. Res. Commun. 186, 277-284, 1992
A:Title: Molecular cloning and sequencing of the gene encoding human angiotensin II type
A:Reference number: J01402; MUID:92181475
A:Accession: J01402
A:Molecule type: DNA
A:Residues: 1-359 <MAU>
R:Furuta, H.; Guo, D.F.; Inagami, T.
Biochem. Biophys. Res. Commun. 183, 8-13, 1992
A:Title: Molecular cloning and sequencing of the gene encoding human angiotensin II type
A:Reference number: J01402; MUID:92181475
A:Accession: J01402
A:Molecule type: DNA
A:Residues: 1-359 <FUR>
A:Cross-references: EMBL:Z11162; NID:928709; PID:g28710
A:Experimental source: Lymphocyte
R:Berghs, D.J.; Ellis, C.; Kumar, C.; Nuthallaganti, P.; Kersten, H.; Elshourbagy, N.; G
Biochem. Biophys. Res. Commun. 183, 989-995, 1992
A:Title: Cloning and characterization of a human angiotensin II type 1 receptor.
A:Reference number: JH0574; MUID:92231907
A:Accession: JH0574
A:Molecule type: mRNA
A:Residues: 1-359 <ABR>
A:Cross-references: GB:M87290; NID:g178682; PID:AAA3535.1; PID:g178683
A:Experimental source: Liver
R:Takayanagi, R.; Ohnaka, K.; Sakai, Y.; Nakao, R.; Yanase, T.; Hajli, M.; Inagami, T.; F
Biochem. Biophys. Res. Commun. 183, 910-916, 1992
A:Title: Molecular cloning, sequence analysis and expression of a cDNA encoding human ty
A:Reference number: JH0267; MUID:92198490
A:Accession: JH0267
A:Molecule type: mRNA
A:Residues: 1-359 <TRK>
A:Experimental source: Liver
R:Currow, K.M.; Pascoe, L.; White, P.C.
Mol. Endocrinol. 6, 1113-1118, 1992
A:Title: Genetic analysis of the human type-1 angiotensin II receptor.
A:Reference number: A44014; MUID:92375105
A:Accession: A44014
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-359 <CUR>
A:Cross-references: GB:M93394; NID:g178680; PID:g178681
A:Note: Sequence extracted from NCBI backbone (NCBI:111831, NCBI:111833)
C:Genetics:
A:Gene: GDB:ACR1
A:Cross-references: GDB:132359; OMIM:106165
A:Map position: 3q21-3q25
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; hormone receptor; transmembrane pr
F:30-53/Domain: transmembrane #status predicted <TM1>

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F:65-90/Domain: transmembrane #status predicted <TM2>
F:103-124/Domain: transmembrane #status predicted <TM3>
F:145-167/Domain: transmembrane #status predicted <TM4>
F:194-216/Domain: transmembrane #status predicted <TM5>
F:241-264/Domain: transmembrane #status predicted <TM6>
F:281-305/Domain: transmembrane #status predicted <TM7>
F:4,176,188/Binding site: carbonylate (Asn) (covalent) #status predicted

Query Match      18.1%; Score 321; DB 2; Length 359;
Best Local Similarity 28.7%; Pred. No. 3,3e-20;
Matches 92; Conservative 56; Mismatches 139; Indels 34; Gaps 9;

QY      26 VIFWINEFLIVCYTLITTELKELYSVTRGVKVRKKVKNKVF-IIAVEFICVPEHF 84
      29 VIFWINEFLIVCYTLITTELKELYSVTRGVKVRKKVKNKVF-IIAVEFICVPEHF 88
Db      85 AKLTGPELRTFVCOVNVVIFETWYISISFLGLITDRYOKTRPRTSNPKNLGAKIL 144
      89 AMEYRMPFENYCKIKASVSVFNLVAVFLLCTSIDRYLAIVHPKSRRLRRTMLVAKYT 148
QY      145 SVYVAFMFLSLPNNIILN-RQPRDKNVKCSF-----LKSERGLVHETLVYICQ 195
      149 CIIIMLAGLASPAIIRHNFFIENNTITVCAFYHESONSTLPGLGLT-KNIIIGFL-- 205
Db      196 VIFWINEFLIVCYTLITTELKELYSVTRGVKVRKKVKNKVF-IIAVEFICVPEHF 255
      206 ----FPFLIITSLTILMKALKKAVEIOK---NKPRNDIDFKIIMAVLFFEF-----FS 252
QY      256 RIRPYTLISQTRDVF-----DCAENTLTYVKESTMLTSLNACLDPEIFPEFLCKSPFN 308
      253 WIFHGFLEFLVLIQGLGVHDCRIADIVDTAMPITICIAVFNCLNPLFGFLGKKRKY 312
QY      309 LISMLK-CPNSATSLSDNRK 328
      313 FLOLKYIRPKAKSHSNLSTK 333

RESULT 14
JC5549
heptahelical p2y5-like receptor - human
C:Species: Homo sapiens (man)
C:Date: 02-Sep-1997 #sequence, revision 05-Sep-1997 #text, change 24-Sep-1999
C:Accession: JC5549
R:Janssens, R.; Boeynaems, J.M.; Godart, M.; Communi, D.
Biochem. Biophys. Res. Commun. 236, 106-112, 1997
A:Title: Cloning of a human heptahelical receptor closely related to the p2y5 recepto
A:Reference number: JC5549; MUID:97366605
A:Accession: JC5549
A:Molecule type: DNA
A:Residues: 1-370 <JAN>
A:Cross-references: DBJ:AF005419; NID:g2240034; PID:AMB66322.1; PID:g2240035
C:Superfamily: ATP receptor p2u

Query Match      18.1%; Score 321; DB 2; Length 370;
Best Local Similarity 27.7%; Pred. No. 3,4e-20;
Matches 87; Conservative 67; Mismatches 134; Indels 26; Gaps 9;

QY      7 LLSAPCNTSLCTRDYKITTOVLPPLTYLFFVGLITNGLAMRIF-FOIRKSNFIIFLKN 65
      22 LGNATANNNT-CIVDDSEFKYLNGLAVSYVFIILGLITNSVSLFVFCFMRKRSFALFITN 80
Db      66 TVISDLMLITLPEFKLSAKLGTGLRPFVCOVNVVIFETWYISISFLGLITDRYOK 125
      81 LNAVSDLEFCTLPFKLFYNNR-RHMPFGDTLCKITSGAFITNIGSMFLTLCISVDRELA 139
QY      126 TTRPRTSNPKNLGAKILSVIWAFFMLSLPNNIILN-RQPRDKNVKCSFLEFGL- 184
      140 IYVPRSRITLRRNSAIVACAGWIIIVLSGSIASLST-----TVNNNAITTCFEG-GLS 193
Db      185 --VMEIIVVICOVIFWINEFLIVV----CYTLITTELKELYSVTRGVKVRKKY 234
      111

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Db 194 KRWKTYLSTKTIIEVVGFIPLILNVSCSSVLRTRLRKPTALSIQGN-----KKK 24
Qy 235 NWKEIIIAVEICEVGFPHFARIPYTLISQRPDPCAEKTEILYVKESTLMTLSNACD 294
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 248 LKMTIVHAAVVGCVFYNSLVFLIALVRQAITNCELEFAKIMPIPLCLATLNCFD 307
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 295 PPIYFIFLCKSPFNS 308
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 308 PPIYFIFLCKSPFNS 321
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT	15
A42656	

angiotensin II receptor type 1b (AT3) -rat
N:Alternate names: Angiotensin II receptor chain B
C:Species: Rattus norvegicus (Norway rat)
C:Date: 04-Mar-1993 #sequence
C:Accession: A42656; S20423
J:Sandberg, K.; Ji, H.; Clark, A.J.; Shapira, H.; Catt, K.J.
J: Biol. Chem. 267, 9455-9458, 1992
A:Title: Cloning and expression of a novel angiotensin II receptor subtype.
A:Reference number: A42656; MUID:92250585
A:Accession: A42656
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-359 <SAN>
A:Cross-references: CB:M90065; NID:g202801; PIDN:AAA40704.1; PID:g202802
A:Experimental source: adrenal cortex
A:Note: sequence extracted from NCBI backbone (NCBIN:100262, NCBIPI:100268)
R:Iwata, N.; Inagami, T.
FEBS Lett. 298, 257-260, 1992
A:Title: Identification of two subtypes in the rat type I angiotensin II receptor
A:Reference number: S20423; MUID:92183879
A:Accession: S20423
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-359 <IN>
A:Cross-references: CB:X64052; NID:g57521; PIDN:CAA5410.1; PID:g57522
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match	17.9%	Score 319;	DB 2;	Length 359;
Best Local Similarity	29.6%	Pred. No. 4.9e-20;		
Matches 92; Conservative	54;	Mismatches 137;	Indels 28;	Gaps 10

QY	26	VLPELITLVEFVLLINGL-AMFIQFOIKSNFIEFLKNPYSIDMLTPEPFIISD	84
Db	29	VMIPTLISIIIVGVIIFGNSLVIVIYIYMYMLKIVASFFLLNLALADLCFLLTLEPMAVYT	88
QY	85	AKLTGRLRFVFCOVTSVIFYFTWYISISPLGLITIDRYOKTTRPEKTSNPKMLGAKIL	144
Db	89	AMEYRMPFGNMLCKIASASVFNLYASVPLFLLTCLSIDRYALAIHPMKSRLRPTMLKAVYT	148
QY	145	SVYIMAFMLSLRNMLITNRQ-PRDNVVKCSF-----LKSEFGVLWHEIVANICQ	195
Db	149	CIITIMLAGLASLPAVYIYRNVYFLENINNTIVCAFYHSQNSTLEPIGLGL-KNILGTV-*	205
QY	196	VIFNINFLIVICYTLITLTKELYSRVYFTRGVAKVPRKRVNVKF-IIIAV--FFTCENP	255
Db	206	---FPELITLITSTYLLIMKLKKRKYIOK---NTPR---NDIDIFRIIMAIVLVEFFFSWVP	255
QY	252	FHFARIPYTSIQTRDVEDPCAENLLEFVKSTSLMLTSLNACIDPFIYFPLCKSFSPNSLIS	311
Db	256	HQITFDVLQLOJLINDCELAIDVDRAMPITTCIAFNNCCLNPLRFYGLGKKFFKRYFLQ	315
QY	312	MLK-CPSNATS 321	
Db	316	LKYIIPPTAKS 326	

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GenCore version 4.5
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OW protein - protein search, using sw model

Run on: September 6, 2002, 15:30:42 : Search time 13.4 Seconds

(Without alignments)
988.215 Million cell updates/sec

Title: US-09-827-937A-2

Perfect score: 1778
Sequence: 1 MQAVDNLTSAPGNTSLCTRD.....SODNRKKEDGSDPNEETPM 342

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 10%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	772	43.4	338	K101_HUMAN	Q15391 homo sapien.
2	694	39.0	305	K101_RAT	O35881 ratius norv
3	488	27.4	319	H963_HUMAN	O14626 homo sapien
4	411.5	23.1	375	GPRX_MOUSE	O9166 homo muscicu
5	409.5	23.0	381	GPRX_HUMAN	O9166 homo sapien
6	394	22.2	342	PAFR_HUMAN	P25105 homo sapien
7	392.5	22.1	342	PAFR_CAVPO	P21536 cavia porce
8	379.5	21.3	361	EBI2_HUMAN	P32249 homo sapien
9	367	20.6	345	CLT2_PIG	O35003 sus scrofa
10	366	20.6	341	PAFR_MOUSE	O62035 mus muscicu
11	362	20.4	341	PAFR_RAT	P46002 ratius norv
12	357.5	20.1	308	P215_CHICK	P32250 gallus gall
13	347.5	19.5	346	CLT2_HUMAN	Q35875 homo sapien
14	347.5	19.5	537	P215_XENLA	P79928 xenopus lae
15	344	19.3	309	CLT2_MOUSE	O32061 mus muscicu
16	339.5	19.1	359	CLT2_RAT	O32419 ratius norv
17	339	19.1	359	AG2R_BOVIN	P5104 bos taurus
18	338	19.0	344	P215_HUMAN	P43657 homo sapien
19	334	18.8	359	AG2R_SHEEP	O77550 ovis aries
20	329.5	18.5	339	GPRH_HUMAN	Q13304 homo sapien
21	329	18.5	359	AG2R_HUMAN	Q13725 homo sapien
22	328	18.4	340	CLT1_PIG	O35055 sus scrofa
23	327	18.4	359	AG2R_PIG	P30555 sus scrofa
24	326	18.3	359	AG2R_CANFA	P43240 canis faml
25	325.5	18.3	359	PAR2_MOUSE	P35086 mus muscicu
26	325	18.3	359	AG2R_RABIT	P4976 oryctolagus
27	321	18.1	359	AG2R_HUMAN	P30556 homo sapien
28	320	18.0	359	AG2R_CAVPO	O9166 cavia porce
29	320	18.0	370	P215_HUMAN	Q99677 homo sapien
30	319.5	18.0	365	GPR8_HUMAN	Q15743 homo sapien
31	319	17.9	359	AG2R_RAT	P25095 ratius norv
32	319	17.9	359	AG2S_RAT	P29089 ratius norv
33	318	17.9	359	AG2R_MOUSE	P29754 mus muscicu

34	316.5	17.8	398	1	OPRM_RAT	P33535 ratius norv
35	316	17.8	359	1	AG2S_MOUSE	P29755 mus muscicu
36	316	17.8	377	1	AP1_RAT	O9166 ratius norv
37	316	17.8	397	1	PAR2_RAT	O63645 ratius norv
38	313.5	17.6	380	1	AP1_HUMAN	P33414 homo sapien
39	313.5	17.6	401	1	OPRM_PIG	O95247 sus scrofa
40	312	17.5	359	1	AG2R_BOVIN	O35210 meriones un
41	312	17.5	401	1	OPRM_BOVIN	P79350 bos taurus
42	311	17.5	369	1	PAR3_MOUSE	O08675 mus muscicu
43	310.5	17.5	362	1	AG2R_XENLA	P32303 xenopus lae
44	310.5	17.5	363	1	AG2S_XENLA	P33573 xenopus lae
45	310	17.4	374	1	PAR3_HUMAN	O00254 homo sapien

ALIGNMENTS

RESULT	ID	Human	Standard	PRT	338 AA
AC	K101_HUMAN	Q15391			
DT	15-JUL-1998	(Rel. 36, Created)			
DT	15-JUL-1998	(Rel. 36, Last sequence update)			
DT	30-MAY-2000	(Rel. 39, Last annotation update)			
DE	Probable G protein-coupled receptor KIAA0001.				
GN	KIAA0001.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISUE=Brain marrow;				
RX	MEDLINE=96051387; PubMed=7584026;				
RA	Nomura N., Miyajima N., Sazuka T., Tanaka A., Kawarabayashi Y.,				
RA	Sato S., Nagase T., Seki N., Ishikawa K.-I., Tabata S.;				
RT	"Prediction of the coding sequences of unidentified human genes. I.				
RT	The coding sequences of 40 new genes (KIAA0001-KIAA0040) deduced by				
RT	analysis of randomly sampled cDNA clones from human immature myeloid				
RT	cell line KG-1."				
RL	DNA Res. 1:27-35(1994).				
CC	- FUNCTION: ORPHAN RECEPTOR.				
CC	- SUBCELLULAR LOCATION: Integral membrane protein.				
CC	- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.				
CC	PROBABLE ORTHOLOG OF RAT VTR 15-20.				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -				
CC	the European Bioinformatics Institute. There are no restrictions on its				
CC	use by non-profit institutions as long as its content is in no way				
CC	modified and this statement is not removed. Usage by and for commercial				
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/				
CC	or send an email to license@sib-sib.ch).				
DR	EMBL	D13626	BAA02791.1		
DR	GenBank	GCR 0594			
DR	InterPro	IPR000276	GPCR_Rhodpsn		
DR	Pfam	PF00001	7tm1.1		
DR	PROSITE	PS00237	G_PROTEIN_RECPT_F1_1		
DR	PROSITE	PS00262	G_PROTEIN_RECPT_F1_2		
KW	G-protein coupled receptor; Transmembrane; Glycoprotein.				
FT	DOMAIN	1	29		
FT	TRANSMEM	30	50		
FT	DOMAIN	51	55		
FT	TRANSMEM	56	76		
FT	DOMAIN	77	96		
FT	TRANSMEM	97	117		
FT	DOMAIN	118	139		
FT	TRANSMEM	140	160		
FT	DOMAIN	161	188		
FT	TRANSMEM	189	209		
FT	DOMAIN	210	234		
FT	TRANSMEM	235	255		

FT	DOMAIN	256	278	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	279	299	7 (POTENTIAL).
FT	DOMAIN	300	338	CYTOPLASMIC (POTENTIAL).
FT	CARBOHYD	3	3	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	161	161	N-LINKED (GLCNAC. . .) (POTENTIAL)
SO	SEQUENCE	338 AA;	38971 MM;	8DBEC782C84753D CR664;

Query Match	43.4%;	Score 772;	DB 1;	Length 338;
Best Local Similarity	47.5%;	Pred. No. 3.4e-45;		
Matches 149;	Conservative 60;	Mismatches 105;	Indels 0;	Gaps 0;

[illegible]

Qy 126 TTRPFKTSNKKNLGAKILSVIWMFMLLSLPMILITNRQPRDKNVKKCSFLKSEGLV 185
: | | :: ::|||: | ||::|||: | | ||| |
Db 123 IVKPIMTSFIOVSYSKLLSVIWMMLLAVPMIILITNQSVREVQIKCIELKSELGRK 1822

QY 186 MHEIINYICQVIFWINEELIVICYTTLTKELYRSYVRTRGVGKVERKKVNKKVFIIIAVF 245
::
Db 183 MHKASNYIFAIFWIVELELLIVFTAITKTIKFKSHLKSSRNSTSVKCKSSRNIIESIVVF 242

```
QY 246 FICFPEFHRIPIYTSQTRVDFDCTENTLFEVKESTMLTSLNACLDPEIFYEFLCKSF
|:||||| |:| | | : : : |:| | | : : |:| | | | |
Db 243 FVCVFYHIAIRIPYTSQTEAHYSCQSEILRIYKKEFTLLLSAANVCLDPITYFFLCQPF 302Z
```

QY	306	KNSLISMLKCPNSA	319
Db	303	REILCKKLHIPLKA	316

RESULT	2
K101_RAT	
ID	K101_RAT
STANDARD;	
PRT;	305 AA.

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DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
```

05 *Rattus norvegicus* (Rat).
0C Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
0C Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

RN [1]
RP SEQUENCE FROM N.A.
RA Charlton M.E., Williams A.S., Fogliano M., Sweetnam P.M., Duman R.S.;

CC -1- FUNCTION: ORPHAN RECEPTOR.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
PROTEIN INTERACTIONS: [Interactome](#)

CC
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstat

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CC -----
DR EMBL; U76206; AAB71745.1; -.
DR GCRDB; GCR_2520; -.
DR InterPro; IPR000276; GPCR_rhoGn

DR Pfam: PF00001; 7tm_1; 1.
DR PROSITE: PS00237; G_PROTEIN_RECIP_FL_1; FALSE_NEG.
DR PROSITE: PS50262; G_PROTEIN_RECIP_FL_2; 1.
KW G-protein coupled receptor. Transmembrane; Glycoprotein

FT	DOMAIN	1	29	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	30	50	1 (POTENTIAL).
FT	TRANSMEM	51	76	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	56	75	2 (POTENTIAL).
FT	TRANSMEM	56	76	EXTRACELLULAR (POTENTIAL).
FT	DOMAIN	77	96	3 (POTENTIAL).
FT	TRANSMEM	97	117	3 (POTENTIAL).
FT	TRANSMEM	118	139	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	140	160	4 (POTENTIAL).
FT	TRANSMEM	140	188	EXTRACELLULAR (POTENTIAL).
FT	DOMAIN	161	204	5 (POTENTIAL).
FT	TRANSMEM	189	239	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	210	234	6 (POTENTIAL).
FT	TRANSMEM	235	275	EXTRACELLULAR (POTENTIAL).
FT	DOMAIN	256	278	7 (POTENTIAL).
FT	TRANSMEM	279	299	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	300	305	7 (POTENTIAL).
FT	CARBOHYD	3	3	CYTOPLASMIC (POTENTIAL).
FT	CARBOHYD	161	163	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	163	163	N-LINKED (GLCNAC. . .) (POTENTIAL).
EQ	SEQUENCE	305 AA;	34800 MW;	640646468E8CC7A3 CR664;

Query Match	39.0%	Score 694	DB 1	Length 305
Best Local Similarity	45.2%	Pred. No. 5.1e-40		
Matches 132	Conservative 61	Mismatches 99	Indels 0	Gaps 0

```

QY      4 VDNLSAPGNSLCTRDYKITVLPPLLYTVLFFGLITNGLAMRIEFOIRSRSNFIIFL 63
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1 MDNTTTEPPKQPCRTNLTITQOIIPMLXCVFETGVLLNGISGWIFFIYVPSSKSFIIYL 60

```

Dy 64 KNTVSDLLMITTFPKILSDAKLGTGPIRTFVCQTVSVIPEFTMYISISFLGITIDRY 12
||:::|||||||:::|| ||:::||||| ||:::|| |||
Db 61 KNIVADFLMGLTFFPKVLSDSGLGPWQLNVFVRKVASVIETVMNYYSIAFFGLISFDKY 12

[illegible]

184 LVMHEIVNIICQVLEWNEFLIVACVITLITKELNSIVKIRINGVGKVEPKKVNKVEFLLA 24
 ||: ||: |||| ||:: ||: ||::||::||::||: ||: ||: ||:
 Db 181 RKWHAASNYEVSIFWFLVLLVFMATRKIFRSHLKSCKNSISVKRKSRSNIFSYL 24

Db 241 AFVACFAPYHARIPYTKSQTEGHYSQAKETLLYTKEFTLLLSANVCIDP 292

RESULT	3
H963_HUMAN	
ID	H963_HUMAN
STANDARD;	
PRT;	319 AA.

DT	30-MAY-2000 (Rel. 39, Created)
DT	30-MAY-2000 (Rel. 39, Last sequence update)
DT	16-OCT-2001 (Rel. 40, Last annotation update)

GN H963.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE FROM N.A.

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RX MEDLINE=98036061; PubMed=9370294;
RA Jacobs K.A., Collins-Racie L.A., Colbert M., Duckett M.,
RA Golden-Fleet M., Kelleher K., Kriz R., Lavallee E.R., Merberg D.,
Golden-Fleet M., Collins-Racie L.A., Colbert M., Duckett M.,

RT "A genetic selection for isolating cDNAs encoding secreted proteins.
RL Gene 198: 289-296(1997).
CC -i- FUNCTION: ORPHAN RECEPTOR.
-i- SUBCELLULAR LOCATION: Intracellular membrane protein

CC -| SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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DR EMBL: AF002986; AAC51846.1; .
 DR InterPro: IPR000276; GPCR_Rhodopsin.
 DR Pfam: PF00001; 7tm.1; 1.
 DR PRINTS: PR000237; GPCRHHODPSN.
 DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; 1.
 DR PROSITE: PS0262; G-PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 21
 FT TRANSMEM 22 42
 FT DOMAIN 43 48
 FT TRANSMEM 49 69
 FT DOMAIN 70 89
 FT TRANSMEM 90 110
 FT DOMAIN 111 132
 FT TRANSMEM 133 153
 FT DOMAIN 154 181
 FT TRANSMEM 182 202
 FT DOMAIN 203 224
 FT TRANSMEM 225 245
 FT DOMAIN 246 268
 FT TRANSMEM 269 289
 FT DOMAIN 290 319
 FT CARBOHYD 3
 SQ SEQUENCE 319 AA; 36754 MW; 79B9821C10841114 CRC64;

Query Match 27.4%; Score 488; DB 1; Length 319;
 Best Local Similarity 34.5%; Pred. No. 3.2e-26; Mismatches 125; Indels 26; Gaps 9;

Matches 112; Conservative 62; Mismatches 125; Indels 26; Gaps 9;
 Oy 13 NPSLCRDYKITYVLPFLYLVFVGLITNGLAMRIFFOIRSKSNFI-IFLKNTVISDL 71
 Db 3 NSSEFCPVYVDELP-FYFYFVLFVGLIGSCFATMAFIQKNTNHRVCSTIYLNLITADF 61
 Oy 72 LMLTPPKLISDAKLGTP-LRTFVCOVTSVFYFTWISIFLGLITIDRYOKTRP 129
 Db 62 LMLTLPVKKIVD-LGVAPMKLIFHCQVACLIYINMYSIFLAFVSDICLOLTHS 119
 Oy 130 FKSNNKLLGAKILSVVIAFMFLSLPMMLLNRPQKNVKKCSFLKEEFLVMEI 189
 Db 120 CKIYRIQEPFAMISTVLAVALVPMWMTPIKDIKESNVGCMEFKEFRNMHL 179
 Oy 190 VNYICQVIFWINE-LIVTVCYTLTKELYSYVTRGVGKVP-RKYNVKKVFIIAVEFI 247
 Db 180 TNYICVAIF-LNFSAILLISNCILVIRQLYRN---KDNENYNNKKALINILVTTGII 234
 Oy 248 CAVPFPFARIPYLTSDRDVCTAENTLFYVKESTLMLTSLNCLDPFIYFLCKSEFN 307
 Db 235 CAVPFIHVRIPYLTSDREVTDCSTRSLFKAEATLLAVSNLCFDPILYYHLSKAFRS 294
 Oy 308 SLI-----SMKCPNSA 319
 Db 295 KYTEFASPKETKAQKEKLKCNNA 319

RESULT 4
 GPRY_MOUSE STANDARD; PRT; 375 AA.
 AC Q9RIK6;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Probable G protein-coupled receptor GPR34.
 GN GPR34.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;

OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99326137; PubMed=10395919;
 RA Schöneberg T., Schulz A., Grosse R., Schade R., Henklein P.,
 RT Schulte G., Gudermann T.;
 RL "A novel subgroup of class I G-protein-coupled receptors.";
 RL Biochem. Biophys. Acta 1446:57-70(1999).
 CC - FUNCTION: ORPHAN RECEPTOR.
 CC - SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC - TISSUE SPECIFICITY: BROADLY EXPRESSED.
 CC - SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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DR EMBL: AF081916; AAD50550.2; .
 DR MGD; MGI:1346334; GPR34.
 DR InterPro: IPR000276; GPCR_Rhodopsin.
 DR Pfam: PF00001; 7tm.1; 1.
 DR PRINTS: PR000237; GPCRHHODPSN.
 DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; 1.
 DR PROSITE: PS0262; G-PROTEIN_RECEP_F1_2; 1.
 KW Receptor; G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 54
 FT TRANSMEM 55 75
 FT DOMAIN 76 81
 FT TRANSMEM 82 102
 FT DOMAIN 103 121
 FT TRANSMEM 122 142
 FT DOMAIN 143 164
 FT TRANSMEM 165 185
 FT DOMAIN 186 209
 FT TRANSMEM 210 230
 FT DOMAIN 231 262
 FT TRANSMEM 263 283
 FT DOMAIN 284 303
 FT TRANSMEM 304 324
 FT DOMAIN 325 375
 FT DISULF 120 197
 FT CARBOHYD 21 21
 FT CARBOHYD 29 29
 FT CARBOHYD 35 35
 FT CARBOHYD 193 193
 FT CARBOHYD 288 288
 SQ SEQUENCE 375 AA; 43173 MW; C04E1C1A52521045 CRC64;

Query Match 23.1%; Score 411.5; DB 1; Length 375;
 Best Local Similarity 32.0%; Pred. No. 4.8e-21; Mismatches 154; Indels 9; Gaps 7;

Matches 101; Conservative 52; Mismatches 154; Indels 9; Gaps 7;

Oy 2 QAVNLTSAFGNTSLCTRDYKITOVLEPLLYLVFVGLITNGLAMRIFFOIRSKSNFI- 60
 Db 25 QASQNSGVPNVT-S-CPMDEKLSTVLTFTFYSVIFVGLVGNITALLYVGLIHRKNSIO 83
 Oy 61 IFLKNTVTSIDLMITLFPKILSDAKLGTP-LRTFVCOVTSVFYFTWISIFLGLITI 120
 Db 84 IYLVNVAADLLIFCLPFRIMHINONKWTGVLICKVAGTLEVMNMYSITILLFPISL 143
 Oy 121 DRYOKTRPFTKSNPKNLGAKILSVVIAFMFLSLPMMLLNRPQKNVKKCSFLKS 180
 Db 144 DRYIINISIQGRRAITTKOSIYVCIWTF-VALAGFLMILITLTKGKNSIMCHYRD 202
 Oy 161 EFGLVWHEIVNTICQVIFWINEFLIYVCTYTLTKELR-SYVTR--GVGKVPKRVNKA 237
 Db 203 RHNAGEAIFNVLVVMFWLILLLITLSYIKGNLRLTSKRSKSPNPGKYATTAARN-- 260

RESULT **5**

```
OY      238 VETIIAIVEICEVPEPHAFIRIPYTTLISQTFDVEDCAENELTVEFKSTSLMTLSYNCLDPFI    297
           ||:::|||||||::||::||::||::||::||::||::||::||::||::||::||::||::||:
Db       261 SFIVLLITTCIFCEPAPHARFRIYISSQLNWSSCIWKKEIHTNLTMLTVSFNSCLDPVM     319
OY      298 YFFLCKSPRNLISM.L 313
           ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||:
Db       320 YFLMSSNRKIMCOLL 335
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GPRY_HUMAN STANDARD; PRT; 381 AA.

ID GPRY_HUMAN
AC O9UPC5; O9S853;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 01-MAR-2002 (Rel. 41, Last annotation update)
DE Probable G protein-coupled receptor GPR34.
GN GPR34.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;

[1]
RN SEQUENCE FROM N.A.
RP TISSUE=Fetal brain;
RX MEDLINE=99326137; PubMed=10395919;
RA Schoneberg T., Schultz A., Grosse R., Schade R., Henklein P.,
RT Schultz G., Gudermann T.;
RL "A novel subgroup of class I G-protein-coupled receptors.";
RN Blochim. Biophys. Acta 1446:57-70(1999).

[2]
RN SEQUENCE FROM N.A.
RP MEDLINE=99156852; PubMed=10036181;
RX Marchese A., Sawadogo M., Nguyen T., Cheng R., Heng H.H., Nowak T.,
RA Im D.-S., Lynch K.R., George S.R., O'Dowd B.F.;
RT "Discovery of three novel orphan G-protein-coupled receptors.";
RL Genomics 56:12-21(1999).

[3]
RN SEQUENCE FROM N.A.
RP MEDLINE=20434921; PubMed=10982042;
RX Jacobl F.K., Broghammer M., Pesch K., Zrenner E., Berger W.,
RA Meindl A., Pusch C.M.;
RT "Physical mapping and exclusion of GPR34 as the causative gene for
RL congenital stationary night blindness type 1.";
RN Hum. Genet. 107:89-91(2000).

[4]
RN SEQUENCE FROM N.A.
RP TISSU=Placenta;
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Tanishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H.,
RA Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K.,
RA Arima M., Nabekura T., Ishii S., Kawai Y., Satoh K., Yamamoto J.,
RA Wakamatsu A., Nakamura Y., Nagahari K., Masuno Y., Oshtina A.;
RT "NEBO human cDNA sequencing project."
RL Submitted (MAY-2001) to the EMBL/Genbank/DBJ databases.

- FUNCTION: ORPHAN RECEPTOR.
- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
- TISSUE SPECIFICITY: BROADLY EXPRESSED.
- SIMILARITY: BELONGS TO FAMILY I OF G-PROTEIN COUPLED RECEPTORS.

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CC or send an email to license@isb-sib.ch).

DR EMBL; AF039686; AAD50531.1; -
DR EMBL; AF118670; AAD17248.1; -
DR EMBL; AK027780; BAB55362.1; -
DR MIM; 300241; -
DR InterPro; IPRO000276; GPCR_Rhodpsn.

[illegible]

RP SEQUENCE FROM N.A.
 RA MEDLINE-92028922; PubMed-16556963;
 RX Ye R.D., Prossnitz E.R., Zou A., Cochran C.G.;
 RT "Characterization of a human cDNA that encodes a functional receptor
 for platelet activating factor.";
 RL Biochem. Biophys. Res. Commun. 180:105-111(1991).
 RN (2)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Leukocytes;
 RX MEDLINE-92041873; PubMed-16579923;
 RA Nakamura M., Honda Z., Izumi T., Sakanaka C., Mutoh H., Minami M.,
 RA Bito H., Sawayama Y., Matsumoto T., Noma M., Shimizu T.;
 RT "Molecular cloning and expression of platelet-activating factor
 receptor from human leukocytes.";
 RL J. Biol. Chem. 266:20400-20405(1991).
 RN (3)
 RP SEQUENCE FROM N.A.
 RX MEDLINE-92250505; PubMed-1374385;
 RA Kunz D., Gerard N.P., Gerard C.;
 RT "The human leukocyte platelet-activating factor receptor. cDNA
 cloning, cell surface expression, and construction of a novel
 epitope-bearing analog.";
 RL J. Biol. Chem. 267:9101-9106(1992).
 RN (4)
 RP SEQUENCE FROM N.A.
 RX MEDLINE-92347886; PubMed-1322356;
 RA Seyffied C.E., Schweickart V.L., Godiska R., Gray P.W.;
 RT "The human platelet-activating factor receptor gene (PTAFR) contains
 no introns and maps to chromosome 1.";
 RL Genomics 13:832-834(1992).
 RN (5)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Heart;
 RX MEDLINE-93112021; PubMed-1281995;
 RA Sugimoto T., Tsuchimochi H., McGregor C.G., Mutoh H., Shimizu T.,
 RA Kurachi Y.;
 RT "Molecular cloning and characterization of the platelet-activating
 factor receptor gene expressed in the human heart.";
 RL Biochem. Biophys. Res. Commun. 189:617-624(1992).
 RN (6)
 RP SEQUENCE FROM N.A.
 RA Benal R.H., Debussche M.S., Olson M.S.;
 RL Submitted (xxx-1992) to the EMBL/GenBank/DBJ databases.
 RN (7)
 RP SEQUENCE FROM N.A.
 RX MEDLINE-93192035; PubMed-8383507;
 RA Chase P.B., Halonen M., Regan J.W.;
 RT "Cloning of a human platelet-activating factor receptor gene:
 evidence for an intron in the 5'-untranslated region.";
 RL Am. J. Respir. Cell Mol. Biol. 8:240-244(1993).
 CC -1- FUNCTION: RECEPTOR FOR PLATELET ACTIVATING FACTOR, A CHEMOTACTIC
 PHOSPHOLIPID MEDIATOR THAT POSSESSES POTENT INFLAMMATORY, SMOOTH-
 MUSCLE CONTRACTILE AND HYPOTENSIVE ACTIVITY. SEEM TO MEDIATE ITS
 ACTION VIA A G PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-
 CALCIN SECOND MESSENGER SYSTEM.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC -----
 DR EMBL: M80436; AAA60001.1; -
 DR EMBL: M76674; AAA60002.1; -
 DR EMBL: D10202; BAA01050.1; -
 DR EMBL: M88177; AAA60214.1; -
 DR EMBL: S52624; AAB24693.2; -
 DR EMBL: L07334; AAA60108.1; -
 DR EMBL: S56396; AAB25755.1; -

DR PIR: JH0479; JH0479.
 DR PIR: A40191; A40191.
 DR PIR: A41079; A41079.
 DR GCRDb: GCR_0186; -
 DR GCRDb: GCR_0260; -
 DR GCRDb: GCR_0285; -
 DR GCRDb: GCR_0414; -
 DR GCRDb: GCR_0478; -
 DR GCRDb: GCR_0548; -
 DR GCRDb: GCR_0731; -
 DR MIM: 173393; -
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR01153; PARRECEPTOR.
 DR PROSITE: PS00237; G_PROTEIN_REC_P1.1;
 DR PROSITE: PS0262; G_PROTEIN_REC_P1.2; 1.
 DR G-protein coupled receptor; Transmembrane; Glycoprotein; Chemotaxis;
 KW Polymorphism.
 FT DOMAIN 1 16
 FT TRANSSEM 17 38
 FT DOMAIN 39 54
 FT TRANSSEM 55 74
 FT DOMAIN 75 91
 FT TRANSSEM 92 113
 FT DOMAIN 114 133
 FT TRANSSEM 134 155
 FT DOMAIN 156 184
 FT TRANSSEM 185 205
 FT DOMAIN 206 233
 FT TRANSSEM 234 254
 FT DOMAIN 255 276
 FT TRANSSEM 277 296
 FT DOMAIN 297 342
 FT DISULFID 90 173
 FT CARBOHYD 169 169
 FT VARIANT 224 224
 FT VARIANT 338 338
 FT VARIANT 338 338
 FT CONFLICT 28 28
 FT CONFLICT 66 66
 FT CONFLICT 95 95
 FT CONFLICT 227 228
 FT CONFLICT 227 228
 FT CONFLICT 247 247
 FT CONFLICT 316 316
 SO SEQUENCE 342 AA; 39203 MW; 890073C9EBA79228 CRC64;
 Query Match 22.2%; Score 394; DB 1; Length 342;
 Best Local Similarity 32.6%; Pred. No. 6; 6e-20;
 Matches 107; Conservative 61; Mismatches 134; Indels 26; Gaps 10;
 QY 11 PONTSLCTDYKYITQVLFPLTYLVLEFVGLITNGLAMRIFQOR--SKSNFI--IFLKNTY 67
 DB 3 PHDSIMDSERFT--LFEIVYSIIIFVLIVAGYVLMWFAFLPKCKEIKETIEMVNL 60
 QY 68 ISDLMLILFFPKILSDAKIGTGLRTFCOVSVIFEFMYISIFLGIITDRYQKT 127
 DB 61 MADMFLFLPLMLIYVYQNGMILPKFLCNVAGCLFINTYISVAFVLTITNRRQAVT 120
 QY 128 RFKPTSNPNLGLAKILSVIV-----AFMFLSLPNMILTNROPDRK--NVKCKSELK 179
 DB 121 RPKITQANTRKRGISLSLVIVWAIYGAASYFLILDS--TNTVPDSAGSGNVTGRC-FEH 176
 QY 180 SEGLVWEIYVANTICOVITMINFLIYVICYTLTKELKRSYVTRGVGKPKRKVNVKVF 239
 DB 177 YEKGSVPVLIHIFEFSEFVFLILFCNLVITRFLMPOVOORNAEVRRLMW-VC 235
 QY 240 IIAVFFICVPPHFAIRIVYTLISOTRDVPCCTAENTLIFYKESTIMLTSLNACLDPIYF 299
 DB 236 TVLAVFTICVPHHVLPVLTIAEL-GFODSKRHOAINDAHOYTLCILSLNCVLDPIYIC 294

QY 300 FLCKSEFN-----SLISMCKPNSAT 320
 Db 295 FLTKFRKHLTEKFSYMSRSSKCRSRT 322

RESULT 7

PAFR_CAVPO STANDARD: PRT: 342 AA.
 AC P21556;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Platelet activating factor receptor (PAF-R).
 GN PAFR.
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
 OX NCBI_TaxID=10141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RX MEDLINE=91101726; PubMed=1846231;
 RA Honda Z.-I., Nakamura M., Miki I., Minami M., Watanabe T., Seyama Y.,
 RA Okada H., Toh H., Ito K., Miyamoto T., Shimizu T.;
 RT "Cloning by functional expression of platelet-activating factor
 RT receptor from guinea pig lung."
 RL Nature 349:342-346(1991).
 CC -1- FUNCTION: RECEPTOR FOR PLATELET ACTIVATING FACTOR. A CHEMOTACTIC
 CC PHOSPHOLIPID MEDIATOR THAT POSSESSES POTENT INFLAMMATORY, SMOOTH-
 CC MUSCLE CONTRACTILE AND HYPOTENSIVE ACTIVITY. SEEM TO MEDIATE ITS
 CC ACTION VIA A G PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-
 CC CALCIUM SECOND MESSENGER SYSTEM.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL: X56736; CAA4060.1; -
 DR PIR: S13638; S13638.
 DR GCRDB: GCR_0034; -
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm.1; 1.
 DR PRINTS: PR01153; PAFRCEPDR.
 DR PROSITE: PS00237; G-PROTEIN_RECPEP_F1_1; 1.
 DR PROSITE: PS50262; G-PROTEIN_RECPEP_F2_1; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Chemotaxis.
 FT DOMAIN 1 16 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 17 18 1 (POTENTIAL).
 FT DOMAIN 19 34 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 35 54 2 (POTENTIAL).
 FT DOMAIN 55 74 2 (POTENTIAL).
 FT TRANSMEM 75 91 3 (POTENTIAL).
 FT DOMAIN 92 113 3 (POTENTIAL).
 FT TRANSMEM 114 133 4 (POTENTIAL).
 FT DOMAIN 134 155 5 (POTENTIAL).
 FT TRANSMEM 156 184 6 (POTENTIAL).
 FT TRANSMEM 185 205 7 (POTENTIAL).
 FT TRANSMEM 206 233 6 (POTENTIAL).
 FT TRANSMEM 234 254 6 (POTENTIAL).
 FT TRANSMEM 255 276 7 (POTENTIAL).
 FT TRANSMEM 277 296 7 (POTENTIAL).
 FT DOMAIN 297 342 7 (POTENTIAL).
 FT CARBOHYD 4 4 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 169 169 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DISULFID 90 173 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT BY SIMILARITY.
 SQ SEQUENCE 342 AA: 38984 MW: B6413B3A5C67B175 CRC64;

Query Match 22.1%; Score 392.5; DB 1; Length 342;
 Best Local Similarity 30.7%; Pred. No. 8.3e-20;
 Matches 103; Conservative 66; Mismatches 146; Indels 21; Gaps 9;

QY 20 DKRTQVLEPLLTYLVEFGLITNGLAMIFQI--RSKSNFI-IFLKNVTSIDLMILT 76
 Db 10 DSEFRTEPLFIYVSIIFGLIANGVYLVWFARLYPSKRIINEIKIFVNLTVADLLEFLT 69
 QY 77 FPKKILSDAKLGPRPLTVCOVTSVIFPTMTIISFGLITLTDKQKTRPKSNPK 136
 Db 70 LPLMTIYVSNQGWFLPKPLCNLAGCLFPIYTCVSAFLGVIITVYNRQAVKPIKTAQAT 129
 QY 137 NLGAKILSVTL-----FMFLSLIPNMLITNRPDRKKVKKCSFLKSEFG-----LVMH 187
 Db 130 TRRGIALSLIVWALVAASVTLVWDSITVSNKKGSGNITGC-FEHYKSGKPVLIIT 188
 QY 188 ELVNYTCQVI-FWINEFLIVCYTLITKELYSVYTRGVKVRKRVKVFIIIAVFF 246
 Db 189 -----ICIVLGFPIVFLLEFCNLVLIHTLRQPVKQQRNAEV-RRRALMNVCTVLAFFV 242
 QY 247 ICFVPRHFARIPYTLISQTDVDCETAEINLFYKESTIMLTSLNACLDPIIYFLCKSFR 306
 Db 243 ICFVPRHNVQLEPTLAEI-GMPSSNHQAINDAHQVTLCLSTNCVLDPIVYCFLTRKFR 301
 QY 307 NSLISMCKPNSATSLSDNRRKKEODGDPNDETPM 342
 Db 302 KHLSEKLNIMRSQKCSRYTDTGTETMAIPINHTPV 337

RESULT 8

EB12_HUMAN
 ID EB12_HUMAN STANDARD: PRT: 361 AA.
 AC P32249;

DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE EBV-Induced G protein-coupled receptor 2 (EBI2).
 GN EB12.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93188173; PubMed=8383238;
 RA Birkenbach M.P., Josefsen K., Yalamanchili R.R., Lenoir G.M.,
 RA Kieff E.;
 RT "Epstein-Barr virus-induced genes: first lymphocyte-specific G
 RT protein-coupled peptide receptors.";
 RL J. Virol. 67:2209-2220(1993).
 CC -1- FUNCTION: ORPHAN RECEPTOR. PROBABLE MEDIATOR OF EBV EFFECTS ON B
 CC LYMPHOCYTES OR OF NORMAL LYMPHOCYTE CELL LINES.
 CC -1- TISSUE SPECIFICITY: B-LYMPHOCYTE CELL LINES.
 CC -1- INDUCTION: BY EBV.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -1- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-5 IS THE INITIATOR.
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL: L08177; AAA35924.1; -
 DR PIR: B45680; B45680.
 DR GCRDB: GCR_0499; -
 DR MIM: 605741; -
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm.1; 1.
 DR PRINTS: PR00237; GPCR_RHODOPSN.

CLUT2_PIG	CLUT2_PIG	STANDARD:	PRT:	345 AA.
ID	CLUT2_PIG			
AC	Q95N03.			
DT	01-MAR-2002 (Rel. 41, Created)			
DT	01-MAR-2002 (Rel. 41, Last sequence update)			
DT	01-MAR-2002 (Rel. 41, Last annotation update)			
DE	CysteinyI leukotriene receptor 2 (CysLTR2).			
GN	CysLTR2 OR CysLTR.			
OS	Sus scrofa (pig).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.			
OX	NCBI_TaxID=9823;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Kamohara M., Takasaki J., Matsumoto M., Matsumoto S., Saito T.,			
RA	Ohishi T., Soga T., Matsushime H., Furuchi K.;			

Db 302 NPFLYYFAGENFKDRLKSA LR 322

```

RESULT 10
PAFR_MOUSE STANDARD: PRT: 341 AA.
ID PAFR_MOUSE 062035;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Platelet activating factor receptor (PAF-R).
GN PAFR.
OS Mus musculus (Mouse).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SV;
RX MEDLINE=9629129; PubMed=8670084;
RA Ishii S., Matsuda Y., Nakamura M., Waga I., Kume K., Izumi T.,
RA Noma M., Shimizu T.;
RT "A murine platelet-activating factor receptor gene: cloning,
RT chromosomal localization and up-regulation of expression by
RT lipopolysaccharide in peritoneal resident macrophages.";
RL Biochem. J. 314:671-678(1996).
CC -1- FUNCTION: RECEPTOR FOR PLATELET ACTIVATING FACTOR, A CHEMOTACTIC
CC PHOSPHOLIPID MEDIATOR THAT POSSESSES POTENT INFLAMMATORY, SMOOTH-
CC MUSCLE CONTRACTILE AND HYPOTENSIVE ACTIVITY. SEEM TO MEDIATE ITS
CC ACTION VIA A G PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-
CC CALCIUM SECOND MESSENGER SYSTEM.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC
CC EMBL: D50872; BAA09468.1; -.
CC GCRDB: GCR_1618; -.
DR GMD: MGI:106066; Pfaff.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS: PRO1153; PAFRECEPTOR.
DR PROSITE: PS00237; G_PROTEIN_RECP_FL_1; 1.
DR PROSITE: PS50262; G_PROTEIN_RECP_FL_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Chemotaxis.
FT DOMAIN 1 16 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 17 38 1 (POTENTIAL).
FT DOMAIN 39 54 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 55 74 2 (POTENTIAL).
FT DOMAIN 75 91 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 92 113 3 (POTENTIAL).
FT DOMAIN 114 133 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 134 155 4 (POTENTIAL).
FT DOMAIN 156 184 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 185 205 5 (POTENTIAL).
FT DOMAIN 206 233 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 234 254 6 (POTENTIAL).
FT DOMAIN 255 275 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 276 295 7 (POTENTIAL).
FT DOMAIN 296 341 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 4 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 169 169 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 90 173 BY SIMILARITY.
SO SEQUENCE 341 AA; 39148 MW; CA8CDBDD8D26937 CRC64;

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Query Match

20.68; Score 366; DB 1; Length 341;

```

Best Local Similarity 29.9%; Pred. No. 4.9e-18;
Matches 96; Conservative 64; Mismatches 133; Indels 28; Gaps 10;

OY 20 DKITQVLEPLLYTVLEFVGLTNGLAMRIEFOI--RSSSNI-IFLKNVTSDDLMIIL 76
   1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 10 DSEFRTLEPIIVSYIFILGVANGVLMVFNALPSKRLNEKIFMVLTMADLLFLFT 69
   1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 77 PPEKLSAKLGTGLRFEVCQVTSVIEFTMYISISFGLITIDRCKTRPFKSNPK 136
   1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 70 LPLWLYVYNNEDWLLPNFLCNVACGLFFINVCSAFLGVTIYNKQAVAPDKRQAT 129
   1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 137 NLGAKILSVYIWM-----FLSLPNMILITNRQPRDKNVKCSFLKSEFG--LWHE 188
   1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 130 TFRKGISLIIWASIVATASVFLATDSTNLVFNKDGSGNITRCFEPHYEPIVAVHY 189
   1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 189 IVNYICQVTFWTFEL-VIVCTLTITKELYSRVRRGKGVKPKRVNVKVFIIIVFET 247
   1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 190 FLAFCEFLVFLIFCNVLIHTLITQPMRQO--RKAGV---KRALMMVCTVLAIVFTI 243
   1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 248 CVPFHFAPIPTLSOTRVDCTAENTLFYVKESTPLMTSLNACDPEIFYFLCKSFKN 307
   1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 244 CVPFHVVQVLPFTLAEIG--YQTNHQAIINDAHQITLCLSTNCVDPVITCETKKFR 301
   1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 308 -----SLISMKCPNSATS 321
   1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 302 HSEKFYSMRSSRK-SRATS 321
   1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 11
PAFR_RAT STANDARD: PRT: 341 AA.
ID PAFR_RAT P46002;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Platelet activating factor receptor (PAF-R).
GN PAFR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=spleen;
RX MEDLINE=94222063; PubMed=8168510;
RA Bito H., Honda Z., Nakamura M., Shimizu T.;
RT "Cloning, expression and tissue distribution of rat
RT platelet-activating-factor-receptor cDNA.";
RL Eur. J. Biochem. 221:211-218(1994).
CC -1- FUNCTION: RECEPTOR FOR PLATELET ACTIVATING FACTOR, A CHEMOTACTIC
CC PHOSPHOLIPID MEDIATOR THAT POSSESSES POTENT INFLAMMATORY, SMOOTH-
CC MUSCLE CONTRACTILE AND HYPOTENSIVE ACTIVITY. SEEM TO MEDIATE ITS
CC ACTION VIA A G PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-
CC CALCIUM SECOND MESSENGER SYSTEM.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: PRESENT IN ALMOST ALL ORGANS INCLUDING SPLEEN,
CC SMALL INTESTINE, KIDNEY, LUNG, LIVER AND BRAIN.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC
CC EMBL: U04740; AAA18422.1; -.
CC GCRDB: GCR_0985; -.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS: PRO1153; PAFRECEPTOR.
DR PROSITE: PS00237; G_PROTEIN_RECP_FL_1; 1.

```

DR PROSITE; PS50262; G-PROTEIN_RECEP_FL_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 Chemotaxis.

FT DOMAIN 1 16 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 17 38 1 (POTENTIAL).
 FT DOMAIN 39 54 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 55 74 2 (POTENTIAL).
 FT DOMAIN 75 91 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 92 113 3 (POTENTIAL).
 FT DOMAIN 114 133 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 134 153 4 (POTENTIAL).
 FT DOMAIN 156 184 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 185 205 5 (POTENTIAL).
 FT DOMAIN 206 233 6 (POTENTIAL).
 FT TRANSMEM 234 254 7 (POTENTIAL).
 FT DOMAIN 255 275 7 (POTENTIAL).
 FT TRANSMEM 276 295 7 (POTENTIAL).
 FT DOMAIN 296 341 7 (POTENTIAL).
 FT CARBOHYD 4 4 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 169 169 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DISULFID 90 173 BY SIMILARITY.
 SO SEQUENCE 341 AA; 39204 MW; D0AF7290C3D34A5B CRC64;

Query Match 20.4%; Score 362; DB 1; Length 341;
 Best Local Similarity 28.9%; Pred. No. 9.1e-18;
 Matches 96; Conservative 66; Mismatches 120; Indels 50; Gaps 10;

OY 20 DYKIVTVLPFLTVLTVFVGLITNGLAMRF---FOIRSKSNFIIFLKNTVISDLMLIT 76
 DB 10 DSEFRYTLFPIYVSVIFGLVANGVAVLWVFATLYPSKKLEIKIFVNLTVADLFLFMT 69
 OY 77 FPKRISDAKLTGRLTFRCOVVSVIFFTMYISIFGLITIDRYOKTTRPEKTSMPK 136
 DB 70 LPLMIYVYVNEGDIMIVKFLCNLAGCLFIMTYCSVAFGLYITNRIQAVAPYIKTAQAT 129
 OY 137 NLGAKILSVYNAFM-----FLSLPNNMLITNRPDRKNVKK-----S 176
 DB 130 TRKRGLTSLVIMISIAATASYFLATDSTNVPRKDSGNTICEHEPEYSPILVVI 189
 OY 177 FLKSEGLVWHEIVNTCOVIFWNLIVCYTLITKELYSVYRTRGVKKVPRKKVNV 236
 DB 190 FITSCFELVEF-----LIFCYNNVYI---HTLITRP-----VROQRKEVKKRALMM 233
 OY 237 KVFIIIVFICFVPFHFARIPYLTISOTRDVECTAENTLFYVKESTWMLSLNACIDPF 296
 DB 234 -VCTVLAVFICFVPHVHVOIPMTLAEIG--YQTNHOAINDAHQITLCLSTNCVDPV 290
 OY 297 IYFFELCKSPFN-----SLISMCKCPNSATS 321
 DB 291 IYCFILTKKFKRKHLESEKFRYSRRSKC-SRAITS 321

RESULT 12
 P2Y5_CHICK STANDARD; PRT; 308 AA.
 ID P2Y5_CHICK
 AC P32250;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE P2Y purinoreceptor 5 (P2Y5) (Purineergic receptor 5) (6ml).
 GN P2RY5.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=T-cell;
 RA MEDLINE=9339058; PubMed=8393036;
 RA Kaplan M.H.; Smith D.I.; Sundick R.S.;
 RT Identification of a G protein coupled receptor induced in activated

RT T cells.";
 RL J. Immunol. 151:628-636(1993).
 CC - SUBCELLULAR LOCATION: Integral membrane protein.
 CC - TISSUE SPECIFICITY: INDUCED IN ACTIVATED T-CELLS.
 CC - SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC -----
 DR EMBL; L06109; AA06387.1; -.
 DR HSSP; P34996; IDDD.
 DR GCRDB; GCR_0689; -.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7cm1.1; 1.
 DR PRINTS; PR01157; P2Y5PROCEPT.
 DR PROSITE; PS00237; G-PROTEIN_RECEP_FL_1; 1.
 DR PROSITE; PS50262; G-PROTEIN_RECEP_FL_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Lipoprotein;
 KW Palmitate.

FT DOMAIN 1 16 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 17 43 1 (POTENTIAL).
 FT DOMAIN 44 52 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 53 76 2 (POTENTIAL).
 FT DOMAIN 77 89 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 90 109 3 (POTENTIAL).
 FT DOMAIN 110 130 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 131 151 4 (POTENTIAL).
 FT DOMAIN 152 178 5 (POTENTIAL).
 FT TRANSMEM 179 206 5 (POTENTIAL).
 FT DOMAIN 207 224 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 225 250 6 (POTENTIAL).
 FT DOMAIN 251 269 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 270 289 7 (POTENTIAL).
 FT DOMAIN 290 308 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 5 5 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 281 281 PALMITATE (BY SIMILARITY).
 FT DISULFID 86 165 POTENTIAL.
 SO SEQUENCE 308 AA; 35597 MW; 4214E96933B6F7D CRC64;

Query Match 20.1%; Score 357.5; DB 1; Length 308;
 Best Local Similarity 29.5%; Pred. No. 1.7e-17;
 Matches 87; Conservative 68; Mismatches 125; Indels 15; Gaps 8;

OY 14 TSLCTRDYKITOVLPPLTVLTVFVGLITNGLAMRF-FOIRSKSNFIIFLKNTVISDL 72
 DB 3 SSGSTEDSEFKYTLVGCVEFMFVLGLIANCAVIFFTLKRNNETTYMLMAISDL 62
 OY 73 MLTPEFKLSDAKLTGRLTFVCOVSVIFFTMYISIFGLITIDRYOKTTRPEKT 132
 DB 63 EYFTLPFRKIYTV-VNMPFGDYLCISVLTFTNMGSLIFLTCISVDPLAIVHPFRS 121
 OY 133 SNPKNLGAKILSVYNAFMFLSLPNNML--TNROPDRKNVKK--SFLKSEGLWHE 188
 DB 122 KILFRKRNARIYCAVAVITVLAGSPASFQSTNRQ--NNTQEQTCENPFESHWKTYLSR 180
 OY 189 IYNYICOVIFWNLIVCYTLITKELYSVYRTRGVKKVPRKKVNVKVFIIIVAFIC 248
 DB 181 IYFIEIVGFPIPLINVTGSTMVLTLPKPLTLRS--NLSKKKVLKMFVHLVIFCF 238
 OY 249 FVPEHFRIPYLTISOTRDVFC--TAENTLFYVKESTWMLSLNACIDPEIIEF 300
 DB 239 FVYNYITLILYSILMRQTWINCSVTVAKRMYPV---TLCIAVSNCCDFIYVF 290

RESULT 13
 CLT2_HUMAN

ID CLT2 HUMAN STANDARD; PRT; 346 AA.
AC 09NS75; 09HCO2; 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DE 01-MAR-2002 (Rel. 41, Last sequence update)
DE Cysteinyln leukotriene receptor 2 (CysLTR2) (P55C0146) (HG57) (HPN321).
GN CysLTR2 OR CysLTR2 OR CysLTR2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID:9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Placenta;
RX MEDLINE=20374466; PubMed=10913337;
RA Takasaki J., Kamohara M., Matsumoto M., Saito T., Sugimoto T., Ota T.,
RA Nishikawa T., Kawal Y., Masuno Y., Isogai T., Suzuki Y., Sugano S.,
RA Furuichi K.;
RT "The molecular characterization and tissue distribution of the human
RT cysteinyl leukotriene CysLTR2 receptor";
RL Biochem. Biophys. Res. Commun. 274:316-322(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20459128; PubMed=10851239;
RA Heise C.E., O'Dowd B.F., Figueroa D.J., Sawyer N., Nguyen T.,
RA Im D.-S., Stocco R., Bellefeuille J.N., Abramowitz M., Cheng R.,
RA Williams D.L. Jr., Zeng Z., Liu Q., Ma L., Clements M.K., Coulombe N.,
RA Liu Y., Austin C.P., George S.R., O'Neill G.P., Metters K.M.,
RA Lynch K.R., Evans J.F.;
RT "Characterization of the human cysteinyl leukotriene 2 receptor";
RL J. Biol. Chem. 275:30531-30536(2000).
RN [3]
RP SEQUENCE FROM N.A.
RX PubMed=11093801;
RA Notack H.-P., Wang Z., Zhu Y., Reinscheid R.K., Lin S.H.S.,
RA Civelli O.;
RT "Molecular cloning and characterization of a second human cysteinyl
RT leukotriene receptor: discovery of a subtype selective agonist";
RL Mol. Pharmacol. 58:1601-1608(2000).
RN [4]
RP SEQUENCE FROM N.A.
RA Dunn M.;
RT Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 17-346 FROM N.A.
RA Suga H.;
RT "Homo sapiens cysteinyl leukotriene receptor 1 like receptor";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Receptor for cysteinyl leukotrienes. The response is
CC mediated via a G-protein that activates a phosphatidylinositol-
CC calcium second messenger system. Stimulation by BAY u9773, a
CC partial agonist, induces specific contractions of pulmonary veins
CC and might also have an indirect role in the relaxation of the
CC pulmonary vascular endothelium. The rank order of affinities for
CC the leukotrienes is LTC4 > LTD4 > LTE4.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: Widely expressed, with highest levels in the
CC heart, placenta, spleen, peripheral blood leukocytes and adrenal
CC gland. In lung, expressed in the interstitial macrophages, and
CC slightly in smooth muscle cells.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
CC EMBL: AB038269; BAB03601.1; -
CC DR EMBL: AF254664; AAC17281.1; -
CC DR EMBL: AF279611; AAK69485.1; -
CC DR

DR EMBL: AL137118; CAC29102.1; -
DR EMBL: AB041644; BAB16379.1; -
DR MIM: 605666; -
DR InterPro: IPR004071; CysLeuk_receptor.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR01533; CysLTR2CPTR.
DR PRINTS: PR00237; GPCR_Rhodopsn.
DR PROSITE: PS00262; G-PROTEIN_REC_F1_2; 1. FALSE_NEG.
DR PROSITE: PS00262; G-PROTEIN_REC_F1_2; 1. FALSE_NEG.
DR G-protein coupled receptor; Transmembrane; Glycoprotein.
KW DOMAIN 1 42
FT TRANSMEM 43 63
FT DOMAIN 64 72
FT TRANSMEM 73 93
FT DOMAIN 94 123
FT TRANSMEM 124 144
FT DOMAIN 145 153
FT TRANSMEM 154 174
FT DOMAIN 175 204
FT TRANSMEM 205 225
FT TRANSMEM 226 245
FT TRANSMEM 246 266
FT DOMAIN 267 286
FT TRANSMEM 287 307
FT DOMAIN 308 346
FT DISULFID 111 187
FT CARBOHYD 20 26
FT CARBOHYD 30 36
FT CARBOHYD 181 181
FT SEQUENCE 346 AA; 39635 MW; EBS4A4A2DDCESEEA CRC64;
SQ

Query Match 19.5%; Score 347.5; DB 1; Length 346;

Best Local Similarity 29.0%; Pred. No. 8.6e-17; Matches 93; Conservative 68; Mismatches 129; Indels 31; Gaps 10;

QY 6 NLTSAGNTSLCTRDYKIQVLPFLYTLFEGTLTNGIAMIPIQIRKSNFI-IFLK 64
DB 20 NGTFSSNNRNCRITIE-NFRREFPIYVLIIFMGVANGNGSIYFQPKYKSTSVNVEML 78
QY 65 NTVISDLMTLPPEK-----ILSDAKIGTGPLRTFVQVYVIFFYMTYSISF 114
DB 79 NLAISDLFIISLPFERADYLRGSNMIFGD-----LACRIMSYSLYVMYSIYF 128
QY 115 LGLITDRQKTRTPKTSNPKNLGAKILISVYIMAFMLTSPNMLTRQPRDKVKK 174
DB 129 LTVLSVRFLLAVHPRLLHVTISRSAMWILGCTIWLIMASSI--MLDSGSEQNGSVTS 186
QY 175 GSFLKSEFLVWHEIVNYICQVTFWINFLIVCYTLITKELYSVYRTGVGKYPKK 233
DB 187 CLEL-NLYKIAMQPMNIALVVGCLLPFTLSICVLLIRVLLKVEVPESG-RVSHRK 244
QY 234 VNVKVFITIAVFFICVPPHFAPIPTLSOTRVPFCTAENTLFFYKESTLMLTSLNACL 293
DB 245 ALTTITITLITLIFLCPLPHLTATVHL--TTWKVGLC-KDRLLKALVITLALANACF 300
QY 294 DPEIYFLCKSPFNLSIMLK 314
DB 301 NPLIYFAGEHFKDRKLSALR 321

RESULT 14
P2Y8_XENLA STANDARD; PRT; 537 AA.
AC P79928;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE P2Y purinoceptor 8 (P2Y8).
GN Xenopus laevis (African clawed frog).
OS

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 6, 2002, 15:30:22 ; Search time 28.74 Seconds
(without alignments)
2058.604 Million cell updates/sec

Title: US-09-827-937A-2
Perfect score: 1778
Sequence: 1 MQAVDNLTSAPGNTSLCTR.....SODNRKKEDGDGDPNETPM 342

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: SPREMBL_19:*
2: SP_archaea:*
3: SP_bacteria:*
4: SP_fungi:*
5: SP_human:*
6: SP_invertebrate:*
7: SP_mammal:*
8: SP_mhc:*
9: SP_organelle:*
10: SP_phage:*
11: SP_plant:*
12: SP_rodent:*
13: SP_virus:*
14: SP_vertelbrate:*
15: SP_unclassified:*
16: SP_rvivirus:*
17: SP_bacteriap:*
17: SP_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1778	100.0	342	4	Q9H244
2	1748	98.3	342	6	Q9BGT8
3	1748	98.3	342	6	Q9SKC3
4	1555.5	87.5	347	11	Q9CPV9
5	1528.5	86.0	343	11	Q9EPX4
6	829	46.6	333	4	Q9BPV8
7	794	44.7	337	11	Q9DBI2
8	741.5	41.7	338	11	Q9ESG6
9	699.5	39.3	358	4	Q9GJZ8
10	694.5	39.1	358	4	Q9BZ21
11	685.5	38.6	359	11	Q9BMT7
12	559	31.4	228	6	Q9BE53
13	553.5	31.1	229	4	Q9BYC2
14	448	25.2	176	4	Q9BVI1
15	388.5	21.9	342	6	Q9TVY5
16	387.5	21.8	342	6	Q9GK76

17	368.5	20.7	296	6	Q9TVY6	Q9TVY6 canis fami
18	367	20.6	345	6	Q95N03	Q95N03 sus scrofa
19	365	20.5	342	6	Q9XSD4	Q9XSD4 sus scrofa
20	356	20.0	374	13	Q57466	Q57466 melagris g
21	347.5	19.5	330	4	Q9HCQ2	Q9HCQ2 homo sapien
22	347.5	19.5	346	4	Q9NS75	Q9NS75 homo sapien
23	344	19.3	309	11	Q920A1	Q920A1 mus musculu
24	343	19.3	359	13	Q9PVY7	Q9PVY7 anguilla an
25	339.5	19.1	309	11	Q924T9	Q924T9 ratu
26	338	19.0	359	6	Q9N0U1	Q9N0U1 ovis aries
27	334	18.8	367	4	Q9UE21	Q9UE21 homo sapien
28	328	18.4	340	6	Q95N02	Q95N02 sus scrofa
29	322	18.1	359	11	Q9EP33	Q9EP33 cavia porce
30	321	18.1	359	6	Q9GLN9	Q9GLN9 pan troglod
31	318	17.9	361	11	Q9JIS7	Q9JIS7 mus musculu
32	316	17.8	377	11	Q9JHG3	Q9JHG3 ratu
33	314	17.7	400	6	Q95M54	Q95M54 macaca fasc
34	311	17.5	361	11	Q95811	Q95811 ratu
35	309.5	17.4	298	4	Q9UD26	Q9UD26 homo sapien
36	309.5	17.4	339	11	Q924T8	Q924T8 ratu
37	309	17.4	358	13	Q9PUA0	Q9PUA0 acipenser r
38	309	17.4	454	4	Q9H573	Q9H573 homo sapien
39	308	17.3	400	6	Q9MTW9	Q9MTW9 macaca mula
40	307	17.3	359	11	Q9EOR9	Q9EOR9 meriones un
41	304.5	17.1	339	11	Q9J7J1	Q9J7J1 mus musculu
42	304.5	17.1	352	11	Q99JA4	Q99JA4 mus musculu
43	304.5	17.1	393	11	Q9R1M0	Q9R1M0 mus musculu
44	304.5	17.1	401	11	Q9R1L9	Q9R1L9 mus musculu
45	304.5	17.1	438	11	Q9R0D1	Q9R0D1 mus musculu

ALIGNMENTS

RESULT 1
Q9H244 PRELIMINARY; PRT; 342 AA.
ID Q9H244;
AC Q9H244;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE P2Y12 PLATELET ADP RECEPTOR (G-PROTEIN COUPLED RECEPTOR SP1999)
DE (GI-COUPLED ADP RECEPTOR HOKK3).
GN HOKK3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Carnivora; Homiidae; Homo.
OC NCBI_TaxID=9606;
OX [1]
RN [1]
RP MEDLINE=21037966; PubMed=11196645;
RX MEDLINE=21037966; PubMed=11196645;
RA Hollinger G., Jantzen H.-M., Vincent D., Li G., England L.,
RA Ramakrishnan V., Yang R.-B., Nurdan P., Nurdan A., Julius D.J.,
RA Conley P.B.;
RT "Identification of the Platelet ADP Receptor Targeted by
RT Antithrombotic Drugs.";
RL Nature 409:202-207(2001).
[2]
RN [2]
RP MEDLINE=21269433; PubMed=11104774;
RX MEDLINE=21269433; PubMed=11104774;
RA Zhang F.L., Luo L., Gustafson E., Lachowicz J., Smith M., Qiao X.,
RA Liu Y.-H., Chen G., Pramanik B., Laz T.M., Palmer K., Bayne M.,
RA Momeni F.J. Jr.;
RT "ADP is the cognate ligand for the orphan G protein-coupled receptor
RT SP1999.";
RL J. Biol. Chem. 276:8608-8615(2001).
[3]
RN [3]
RP MEDLINE=21394281; PubMed=11502873;
RX MEDLINE=21394281; PubMed=11502873;
RA Takasaki J., Kamohara M., Saito T., Matsumoto M., Matsumoto S.,
RA Ohishi T., Soga T., Matsushima H., Furuichi K.;
RT "Molecular cloning of the platelet P2YAC ADP receptor";
RT Pharmacological comparison with another ADP receptor, the P2Y1

RT receptor.";
 RL Mol. Pharmacol. 60:432-439(2001).
 DR EMBL: AF313449; AAC48944.1; -;
 DR EMBL: AF321815; AAK00948.1; -;
 DR EMBL: AB052684; BAB60824.1; -;
 DR InterPro: IPR000276; GPCR_Rhodopsin.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCR_Rhodopsin.
 DR PROSITE: PS0262; G_PROTEIN_RECIP_F1_2; 1.
 KW Receptor.
 SQ SEQUENCE 342 AA; 39438 MW; 8553D2746C89176D CRC64;

Query Match 100.0%; Score 1778; DB 4; Length 342;
 Best Local Similarity 100.0%; Pred. No. 3.4e-151;
 Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOAVDNLTSAPGNTSLCTRDYKITQVLEFLLYTVLFEVGLITNGLAMRIFFOIRSKSNFI 60
 DB 1 MOAVDNLTSAPGNTSLCTRDYKITQVLEFLLYTVLFEVGLITNGLAMRIFFOIRSKSNFI 60
 QY 61 IFLKNTVISDLMLILFPFKILSDAKLGTPRTFVCQVTSVIFETMYISISFLGLITI 120
 DB 61 IFLKNTVISDLMLILFPFKILSDAKLGTPRTFVCQVTSVIFETMYISISFLGLITI 120
 QY 121 DRYQKTRPFTSNPKNLGAKILSVYIWAEMFLSLPNMILTNRPDRKNVKKCSFLKS 180
 DB 121 DRYQKTRPFTSNPKNLGAKILSVYIWAEMFLSLPNMILTNRPDRKNVKKCSFLKS 180
 QY 181 EFGLVWHEIYNTICQVIFWINEFLIVCYTLITKELRSYVTRGVGKVPKKNVAVFI 240
 DB 181 EFGLVWHEIYNTICQVIFWINEFLIVCYTLITKELRSYVTRGVGKVPKKNVAVFI 240
 QY 241 IIAVFICVPHFPHARIPYTLISQTRDVPDCTAENTLFEYKESTLMLTSLNACLDPEIYFF 300
 DB 241 IIAVFICVPHFPHARIPYTLISQTRDVPDCTAENTLFEYKESTLMLTSLNACLDPEIYFF 300
 QY 301 LCKSFNLSLSMLKCPNSATSLSDNRKKEODGDPNEETPM 342
 DB 301 LCKSFNLSLSMLKCPNSATSLSDNRKKEODGDPNEETPM 342

RESULT 2
 Q9BGT8 PRELIMINARY; PRT: 342 AA.
 ID Q9BGT8;
 DT 01-JUN-2001 (Tremblrel. 17, Created)
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE HYPOTHETICAL 39.5 KDA PROTEIN.
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Macaca.
 OX NCBI_TaxID=9541;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=FRONTAL LOBE LEFT;
 RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
 RA Suzuki Y., Sugano S., Hashimoto K.;
 RA "Isolation of full-length cDNA clones from macaque brain cDNA
 RT libraries."
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB056385; BAB33041.1; -;
 DR InterPro: IPR000276; GPCR_Rhodopsin.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCR_Rhodopsin.
 DR PROSITE: PS0262; G_PROTEIN_RECIP_F1_2; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 342 AA; 39497 MW; 3D21BF987FC48599 CRC64;

Query Match 98.3%; Score 1748; DB 6; Length 342;

Best Local Similarity 98.0%; Pred. No. 1.6e-148;
 Matches 335; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MOAVDNLTSAPGNTSLCTRDYKITQVLEFLLYTVLFEVGLITNGLAMRIFFOIRSKSNFI 60
 DB 1 MOAVDNLTSAPGNTSLCTRDYKITQVLEFLLYTVLFEVGLITNGLAMRIFFOIRSKSNFI 60
 QY 61 IFLKNTVISDLMLILFPFKILSDAKLGTPRTFVCQVTSVIFETMYISISFLGLITI 120
 DB 61 IFLKNTVISDLMLILFPFKILSDAKLGTPRTFVCQVTSVIFETMYISISFLGLITI 120
 QY 121 DRYQKTRPFTSNPKNLGAKILSVYIWAEMFLSLPNMILTNRPDRKNVKKCSFLKS 180
 DB 121 DRYQKTRPFTSNPKNLGAKILSVYIWAEMFLSLPNMILTNRPDRKNVKKCSFLKS 180
 QY 181 EFGLVWHEIYNTICQVIFWINEFLIVCYTLITKELRSYVTRGVGKVPKKNVAVFI 240
 DB 181 EFGLVWHEIYNTICQVIFWINEFLIVCYTLITKELRSYVTRGVGKVPKKNVAVFI 240
 QY 241 IIAVFICVPHFPHARIPYTLISQTRDVPDCTAENTLFEYKESTLMLTSLNACLDPEIYFF 300
 DB 241 IIAVFICVPHFPHARIPYTLISQTRDVPDCTAENTLFEYKESTLMLTSLNACLDPEIYFF 300
 QY 301 LCKSFNLSLSMLKCPNSATSLSDNRKKEODGDPNEETPM 342
 DB 301 LCKSFNLSLSMLKCPNSATSLSDNRKKEODGDPNEETPM 342

RESULT 3
 Q95KC3 PRELIMINARY; PRT: 342 AA.
 ID Q95KC3;
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE HYPOTHETICAL 39.5 KDA PROTEIN.
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Macaca.
 OX NCBI_TaxID=9541;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=MEDULLA OBLONGATA;
 RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
 RA Suzuki Y., Sugano S., Hashimoto K.;
 RA "Isolation of full-length cDNA clones from macaque brain cDNA
 RT libraries."
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB062981; BAB60747.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 342 AA; 39479 MW; E93FC26BFF5EC4C CRC64;

Query Match 98.3%; Score 1748; DB 6; Length 342;
 Best Local Similarity 98.0%; Pred. No. 1.6e-148;
 Matches 335; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MOAVDNLTSAPGNTSLCTRDYKITQVLEFLLYTVLFEVGLITNGLAMRIFFOIRSKSNFI 60
 DB 1 MOAVDNLTSAPGNTSLCTRDYKITQVLEFLLYTVLFEVGLITNGLAMRIFFOIRSKSNFI 60
 QY 61 IFLKNTVISDLMLILFPFKILSDAKLGTPRTFVCQVTSVIFETMYISISFLGLITI 120
 DB 61 IFLKNTVISDLMLILFPFKILSDAKLGTPRTFVCQVTSVIFETMYISISFLGLITI 120
 QY 121 DRYQKTRPFTSNPKNLGAKILSVYIWAEMFLSLPNMILTNRPDRKNVKKCSFLKS 180
 DB 121 DRYQKTRPFTSNPKNLGAKILSVYIWAEMFLSLPNMILTNRPDRKNVKKCSFLKS 180
 QY 181 EFGLVWHEIYNTICQVIFWINEFLIVCYTLITKELRSYVTRGVGKVPKKNVAVFI 240
 DB 181 EFGLVWHEIYNTICQVIFWINEFLIVCYTLITKELRSYVTRGVGKVPKKNVAVFI 240

OY 241 IIAVFICFVPHFARIPYLTSDRDVDCDAENTLFYVKESTLMTLSLNACDLPFIYEF 300
DB 241 IIAVFICFVPHFARIPYLTSDRDVDCDAENTLFYVKESTLMTLSLNACDLPFIYEF 300
OY 301 LCKSFNLSLMLKCPNSATSLSQDNKKKQDGGDPNEETPM 342
DB 301 LCKSFNLSLMLKCPNSATSLSQDNKKKQDGGDPNEETPM 342

RESULT 4

O9CPV9 PRELIMINARY: PRT: 347 AA.

AC 09CPV9; 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DE 4921504D23RIK PROTEIN (2900079B22RIK PROTEIN).
GN P2RY12 OR 4921504D23RIK OR 2900079B22RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;

RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=TESTIS, AND HIPPOCAMPUS;
MEDLINE=21085660; PubMed=11217851;

RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Alzawa K., Izawa M., Nishii K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuell P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schiml L.M., Staahl F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Oikido T., Furuno M., Aono H., Balderelli R., Barsh G.,
RA Blake J., Boftelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Saeki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitlaker C., Wilmberg L.,
RA Wyszew-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
EMBL: AK014807; BAB29561.1; -;
DB EMBL: AK013804; BAB29000.1; -;
DR MGD: MGI:1918089; P2RY12.
DR MGD: MGI:1920308; 2900079B22RIK.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1
DR PRINTS: PR00237; GPCR_Rhodopsn.
DR PROSITE: PS50262; G_PROTEIN_RECIP_F1_2; 1.
SQ SEQUENCE 347 AA; 39473 MW; F107488E57E025F1 CRC64;

Query Match 87.5%; Score 1555.5; DB 11; Length 347;
Best Local Similarity 88.7%; Pred. No. 2,7e-131;
Matches 299; Conservative 16; Mismatches 21; Indels 1; Gaps 1;

OY 6 NLTSAPGNTSLCTRDYKTIQVLEPLLYTVLFFVGLITNGLAMRIPOIRKSNFIIFLKN 65
DB 12 NTFESGISTFLCVROKTIQVLEPLLYTVLFFVGLITNSLAMRIPOIRKSNFIIFLKN 71
OY 66 TVISDLMLITLFFPKILSDAKLGTPLRTFVCQVSVIYFTMYISISFLGLITIDRYOK 125
DB 72 TVISDLMLITLFFPKILSDAKLGTPLRTFVCQVSVIYFTMYISISFLGLITIDRYOK 131
OY 126 TTRPFTSNPKNLGAKLISVYIWAHMFLLSLPNNMILTNROPDKNKKCSFLKSEGLV 185
DB 132 TTRPFTSNPKNLGAKLISVYIWAHMFLLSLPNNMILTNROPDKNKKCSFLKSEGLV 191

OY 186 WHEIYNYICOVLEWTFINELIVICYTLITKELYRSYVTRGVGVKPKKYNVVFIIIAV 245
DB 192 WHEIYNYICOVLEWTFINELIVICYTLITKELYRSYVTRGVGVKPKKYNVVFIIIAV 251
OY 246 FICFVPHFARIPYLTSDRDVDCDAENTLFYVKESTLMTLSLNACDLPFIYEFICKSF 305
DB 252 FICFVPHFARIPYLTSDRDVDCDAENTLFYVKESTLMTLSLNACDLPFIYEFICKSF 311
OY 306 RNSLSMLKCPNSATSLSQDNKKKQDGGDPNEETPM 342
DB 312 RNSLSMLKCPNSATSLSQDNKKKQDGGDPNEETPM 347

RESULT 5

O9EPX4 PRELIMINARY: PRT: 343 AA.

AC 09EPX4; 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE P2Y12 PLATELET ADP RECEPTOR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;

RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
MEDLINE=21037966; PubMed=1196645;
RA Hollinger G., Jantzen H.-M., Vincent D., Li G., England L.,
RA Ramakrishnan V., Yang R.-B., Nurdan P., Nurdan A., Julius D.J.,
RA Conley P.B.;
RT "Identification of the Platelet ADP Receptor Targeted by
RT Antithrombotic Drugs.";
RL Nature 409:202-207(2001).
EMBL: AF133450; AAC48945.1; -;
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1
DR PRINTS: PR00237; GPCR_Rhodopsn.
DR PROSITE: PS50262; G_PROTEIN_RECIP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 343 AA; 39047 MW; 7AE0AC6E6674136 CRC64;

Query Match 86.0%; Score 1528.5; DB 11; Length 343;
Best Local Similarity 86.9%; Pred. No. 6,9e-129;
Matches 293; Conservative 17; Mismatches 22; Indels 5; Gaps 1;

OY 6 NLTSAPGNTSLCTRDYKTIQVLEPLLYTVLFFVGLITNGLAMRIPOIRKSNFIIFLKN 65
DB 12 NTFESGISTFLCVROKTIQVLEPLLYTVLFFVGLITNSLAMRIPOIRKSNFIIFLKN 71
OY 66 TVISDLMLITLFFPKILSDAKLGTPLRTFVCQVSVIYFTMYISISFLGLITIDRYOK 125
DB 72 TVISDLMLITLFFPKILSDAKLGTPLRTFVCQVSVIYFTMYISISFLGLITIDRYOK 131
OY 126 TTRPFTSNPKNLGAKLISVYIWAHMFLLSLPNNMILTNROPDKNKKCSFLKSEGLV 185
DB 132 TTRPFTSNPKNLGAKLISVYIWAHMFLLSLPNNMILTNROPDKNKKCSFLKSEGLV 191
OY 186 WHEIYNYICOVLEWTFINELIVICYTLITKELYRSYVTRGVGVKPKKYNVVFIIIAV 245
DB 192 WHEIYNYICOVLEWTFINELIVICYTLITKELYRSYVTRGVGVKPKKYNVVFIIIAV 251
OY 246 FICFVPHFARIPYLTSDRDVDCDAENTLFYVKESTLMTLSLNACDLPFIYEFICKSF 305
DB 252 FICFVPHFARIPYLTSDRDVDCDAENTLFYVKESTLMTLSLNACDLPFIYEFICKSF 311
OY 306 RNSLSMLKCPNSATSLSQDNKKKQDGGDPNEETPM 342
DB 312 RNSLSMLKCPNSATSLSQDNKKKQDGGDPNEETPM 343

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RESULT 6
Q9BPV8 PRELIMINARY; PRT; 333 AA.
AC Q9BPV8;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE PUTATIVE G-PROTEIN-COUPLED RECEPTOR FKS677 (G-PROTEIN COUPLED RECEPTOR GPR86) (G PROTEIN-COUPLED RECEPTOR) (G PROTEIN-COUPLED RECEPTOR GPR86)
GN FKS677 OR GPR86 OR GPR94.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HEART;
RA Wang Y., Gong L.;
RT "Molecular cloning of FKS677, a novel gene encoding a putative G-protein-coupled receptor."
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21172992; PubMed=11273702;
RT "An expressed sequence tag (est) data mining strategy succeeding in the discovery of new G-protein coupled receptors."
RL J. Mol. Biol. 307:799-813(2001).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=21458557; PubMed=11574155;
RT Lee D.K., Nguyen T., Lynch K.R., Cheng R., Vantli W.B., Arkhitko O., Lewis T., Evans J.F., George S.R., O'Dowd B.F.;
RT "Discovery and mapping of ten novel G protein-coupled receptor genes."
RL Gene 275:83-91(2001).
RN [4]
RP SEQUENCE FROM N.A.
RX PubMed=11546776;
RA Communi D., Gonzalez N.S., Dethieux M., Brezillon S., Lannoy V., Parmentier M., Boeynaems J.M.;
RT "Identification of a Novel Human ADP Receptor Coupled to G1."
RL J. Biol. Chem. 276:4179-4185(2001).
DR EMBL: AF345565; AAK29068.1; -
DR EMBL: AF295368; AAK01864.1; -
DR EMBL: AF411113; AAL26484.1; -
DR EMBL: AF40692; AAL01038.1; -
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHOOPS.
DR PROSITE: PS00237; G-PROTEIN_RECEP_FL_1; UNKNOWN_1.
DR PROSITE: PS50262; G-PROTEIN_RECEP_FL_2; 1.
KW RECEPTOR.
SQ 333 AA; 38440 MW; F234AB50016DF34 CRC64;

Query Match 46.6%; Score 829; DB 4; Length 333;
Best Local Similarity 49.1%; Pred. No. 2.4e-66;
Matches 153; Conservative 57; Mismatches 102; Indels 2; Gaps 1;

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QY 197 IEMINELIVCYTLITKELRSYVTRGVGKVPKRKVNVKFIILIAVEICFVPEHAR 256
DB 195 IFWYFILLVFFYVIAKAVDSYRKSCKRNNKKLEGKFFVAVVFCAPFHFAR 254
QY 257 IPYTLSDTRVEDCTAENTLFFVKESTLMTLSLACDLPFIYFELCKSFNLSLSMKCP 316
DB 255 VPTYSQNNKNTKDCQLQNOFLFAKETTLFIAATNICMDPLIYFLCKKFTKLPQW--G 312
QY 317 NSATLSQDNKKKED 332
DB 313 RKTATSOENHSSQPD 328

RESULT 7
Q9DB12 PRELIMINARY; PRT; 337 AA.
AC Q9DB12;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE 2010001106RIK PROTEIN.
GN GPR86 OR 2010001106RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=SMALL INTESTINE;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arikawa T., Hara A., Fukunishi Y., Kono H., Adachi S., Fukuda S., Sakai K., Itawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochina H., Kuehl P., Lewis S., Matsuo Y., Nikaio I., Pesole G., Quackenbush J., Schriml L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Williams L., Wyszewski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlsuki S., Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
DR EMBL: AK008013; BAB25409.1; -
DR MGP: MGI:1921441; GPR86.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHOOPS.
DR PROSITE: PS00237; G-PROTEIN_RECEP_FL_1; UNKNOWN_1.
DR PROSITE: PS50262; G-PROTEIN_RECEP_FL_2; 1.
SQ 337 AA; 38693 MW; 2C1A76FBF93D5EA CRC64;

Query Match 44.7%; Score 794; DB 11; Length 337;
Best Local Similarity 45.9%; Pred. No. 3.2e-63;
Matches 151; Conservative 63; Mismatches 111; Indels 4; Gaps 3;

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[illegible]

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AC	Q9ESG6				
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DT	01-MAR-2001	(TREMblrel. 16, Last sequence update)			
DT	01-JUN-2001	(TREMblrel. 17, Last annotation update)			
DE	7 TRANSMEMBRANE G-PROTEIN COUPLED RECEPTOR.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Lee B.C., Scadden D.T.;				
RT	"7 transmembrane G protein coupled receptor from hematopoietic				
RT	progenitors.";				
RL	Submitted (Aug-1999) to the EMBL/GenBank/DBJ databases.				
DR	EMBL, AF177211, AAC09275.1;				
DR	InterPro: IPR000276; GPCR_Rhodpn.				
DR	Pfam: PF00001; 7tm_1; 1.				
DR	PRINTS: PR00237; GPCRHDOPSN.				
DR	ProSITE: PS50262; G-PROTEIN_RECPT_FL_2; 1.				
KW	Receptor; Transmembrane.				
SO	SEQUENCE 338 AA; 3861 MW; 437650622A68A4E CRC64;				

Query Match	41.78;	Score 741.5;	DB 11;	Length 338;
Best Local Similarity	44.18;	Pred. NO. 1.6e-58;		
Matches 146;	Conservative 69;	Mismatches 109;	Indels 7;	Gaps 3;

Qy	4	VDNLTSLPAGNTSLCTBRKYKIQVWFLPILLYVLFVGVGDTITGLMIRIPEFORSSKNFIYL	63
Db	1	MNNSTTDDPNOQPCSMWTLITKOIILPYLYGMVFLITGLLNGISGMWIFFYPPSSKSFIIYL	60
Qy	64	KNYVYISDLMLITLPPFKILSDAKIGTGPRLTPVCQVTSVIFPTMYISISLCLITIDRY	1233
Db	61	KNIVYAFGLMGTLPFRYVLDGSGLPQVWVAFVCRSAVTEFYVMVYSIYFPLISIDRY	1201
Qy	124	QKTRPEKTSNPMLTLAKILSVYIAFMFLSLPNMILINROPDRKNNVKKCSFLKSEFG	1833
Db	121	YKIKPLLTSLVQSVNNSKLLSLVYMMMLMLLLANPNILNLNGQVKEVTKIQCHELNELG	1801
Qy	184	LVHMEIYVIGQVFWINFLIVICYLTITLKELYRSVTRGVGKVPKKVNVKVFIIIA	2433
Db	181	RKMHKASNYIYVSLFWVFLILIVFYATIRKIFKSHLKRKKNSTSVKRRKSSRNIFSIYL	2401
Qy	244	VFFICVFNPFHARIPYTLISQTRDVFCDCTAETNITFYVHESYTLMLTSLWACDPIYFELCK	3033
Db	241	VFVVCVPFYHARIPYTKSQTEGHSYSCRTEIILYIAKEFTLLLSAANVCDDPIIYFELCO	3001
Qy	304	SFR---NSLSM-LKCRNSATSLSDNNRKE	330
Db	301	PFREVLNKKLHMSLKVN---DEVSVKTRK	328

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RESULT      9
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AC      096J28;
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DT      01-DEC-2001 (TREMblrel, 19, Last sequence update)
DT      01-DEC-2001 (TREMblrel, 19, Last annotation update)
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OS      G PROTEIN-COUPLED RECEPTOR.
OC      Homo sapiens (Human) .
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX      NCBI_Taxid=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=PLACENTA;
RA      Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA      Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA      Maetsuna M., Hosoi T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA      Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA      Wakanebe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA      Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuno Y.,
RA      Ninomiya K., Iwayanagi T.;
RT      "NEDO human cDNA sequencing project.";
RL      Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR      EMBL: AK027784; BAB55366.1; -
SO      SEQUENCE      358 AA;      41462 MW;      7822700C8E3CCTE9 CRC64;

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Query Match	39.3%;	Score 699.5;	DB 4;	Length 358;
Best Local Similarity	42.6%;	Pred. No. 9.6e-55;		
Matches 140;	Conservative 67;	Mismatches 113;	Indels 9;	Gaps 5

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Db	25	NRSDPGKNTLL--HNEFDITVLPVLLIFVASILNGLAWAIFPIHINKTSFITYLK	81
QY	65	NTVTSIDMLITLTPFKILSDAKLGTGTPRTVCQVTSVIFETFWYISISPLGTTIDRQ	122
Db	82	NIYVADLLMTLTPFPRIYVHDGFQBPWFKFLCKTSTVLFPANNYTSIVFGLLSIDRYL	143
QY	125	KTRPFTKSNRKNLGAKILSVYIWAEMFLSLSPNMLITNRQPRDKVWKKCSFLKSEGL	184
Db	142	KVNPFGDSRMYNTFTFKVLSVCWVIMAYVLSNIIITLNGQPTREDNIHDCSKLSPGV	203
QY	185	VWHELVNVIQGVIMINFLIYVGYTLITLTKRLSYRTKRYGVKPPK--KYNKVFIIIA	244
Db	202	KWHIAVTVNSCLFVAALVYLITGLCTIALSRHKS--SROFTSOSRRKRKHOSIRVVA	255
QY	244	VEFTCEVDFHFAPIPYTLQSOTRDVFDCTAENTLTVYKVESTLMLTSLNACDIPFIYFLCK	303
Db	260	VEFTCELPYHLCRIDPFESHIDRLDLSAQIILLYCKEITLFLSACNVCIDPIIYFPMCR	319
QY	304	SFRNSLI--SMLKCPNSATLSIQDNKKE	330
Db	320	SFSRRLFKKSNIKTRSESIRSLQSVRSE	348

RESULT	10		
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ID	Q9BYZ1	PRELIMINARY;	PRT; 358 AA.
AC	Q9BYZ1;		
DT	01-JUN-2001 (TREMBLrel. 17, Created)		
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)		
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)		
DE	ORPHAN G PROTEIN-COUPLED RECEPTOR 87.		
GN	GPR87 OR GPR95.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		

RA Yang W.S., Diehl J.R., Roubesh W.E.;
RT "Partial Sequence of Bovine Platelet-Activating Factor Receptor
RT Gene";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA He B., Triemann U., Kanitz W., Weikard R., Laurent P., Schwerin M.,
RA Schmidt P.;
RT "Molecular characterization of bovine platelet-activating factor
RT receptor transcripts and their detection in different tissues of
RT cattle";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF187321; AAF01439.2; .
DR EMBL; AJ295321; CAC43290.1; .
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PROSITE; PS00237; G_PROTEIN_RECIP_F1_1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECIP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 342 AA; 39691 MW; 7C4236205AE937C9 CRC64;

Query Match 21.9%; Score 388.5; DB 6; Length 342;
Best Local Similarity 30.3%; Pred. No. 5.9e-27;
Matches 101; Conservative 63; Mismatches 136; Indels 31; Gaps 10;
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DB 3 PNNFPRDSEPRYT--LPPIYSIVFVGLVANSYVLMVFARLYPSKKFNEIKIFMVNLT 60
QY 68 ISDLMLITPEPKILSDAKLIGTGPLRTFVCOVTSVIEFTMYISISFLGLITIDRYQKTT 127
DB 61 MADLLFVTLPLMIVYYNQGDMILPKFLCNLAGCFEFTNYCSVAFLAVITYNRFQAVT 120
QY 128 RPEKTSNPKNLGAKILSVTW-----AFMFLSLPMLITNRP--DKNVKKCSF 177
DB 121 RPIKTAQATTRKRKILSLILTIWSIVGAASYFEVLD-----STNREPMTGSANITRC-F 174
QY 178 LKSEGLVMEHIEIVNYICOVIFWINEFLIYVCYTLITKELYRSYVRTRGVKKRVNVK 237
DB 175 EHYEKGSIPVLTIIHFLVFSFVLVFLITLPCNLVITIRTLTQQVOIQRNAEYKRRLMM- 233
QY 238 VEITIAVFFICFVPPHAFRIPYTUSQTRDVPDCTAENTLFYVKESTLMLTSLNACLDPEI 297
DB 234 VCVLAVFIIICFVPHHIVOLPWLAEI-GFQDTEHQAINDAHQVTLCLLSTNCVLDPII 292
QY 298 YEFICKSFRNLSLML-----KCPNSATS 321
DB 293 YCFLLKKFRKHLTEKLYSMRESRC-SRATS 322

Search completed: September 6, 2002, 15:34:20
Job time: 238 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 6, 2002, 15:28:27 ; Search time 13.07 Seconds
(without alignments)
639.139 Million cell updates/sec

Title: US-09-827-937A-2

Perfect score: 1778
Sequence: 1 MQAVDNLTSAFGNTSLCTRD.....SQDNRRKKEDGGDPNEETPM 342

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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4: /cgn2_6/prodata/2/1aa/6B-COMB.pep:*
5: /cgn2_6/prodata/2/1aa/PCrUS-COMB.pep:*
6: /cgn2_6/prodata/2/1aa/backfillset1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	823	46.3	333	4	US-09-221-456-2
3	823	46.3	333	4	US-09-558-740-2
4	797	43.4	333	2	US-08-812-871-1
5	772	43.4	325	2	US-08-467-948A-29
6	772	43.4	325	3	US-08-467-947A-29
7	772	43.4	338	3	US-08-988-876-8
8	772	43.4	338	4	US-09-303-524A-2
9	679.5	38.2	358	3	US-08-988-876-3
10	546.5	30.7	293	2	US-08-467-948A-6
11	546.5	30.7	293	3	US-08-467-947A-6
12	488	27.4	326	1	US-08-702-344-28
13	410.5	23.1	326	1	US-08-118-270-39
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17	379.5	21.3	361	1	US-08-352-678-4
18	379.5	21.3	361	5	PCT-US93-08636-4
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20	374.5	21.1	381	1	US-08-467-125-2
21	374.5	21.1	381	2	US-08-911-320A-2
22	374.5	21.1	381	4	US-09-217-101-2
23	349.5	19.7	302	2	US-08-467-948A-30
24	349.5	19.7	302	3	US-08-467-947A-30
25	339	19.1	344	2	US-08-467-948A-8
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27	337	19.0	68	4	US-08-905-223-327

28	329.5	18.5	339	1	US-08-153-848-44	Sequence 44, Appl
29	329.5	18.5	339	2	US-08-812-871-3	Sequence 3, Appl
30	329.5	18.5	339	2	US-09-299-843A-44	Sequence 44, Appl
31	329.5	18.5	339	4	US-09-088-337B-44	Sequence 44, Appl
32	329.5	18.5	339	5	PCT-US93-11153-44	Sequence 44, Appl
33	329.5	18.5	339	5	PCT-US95-07180-2	Sequence 6, Appl
34	329	18.5	359	1	US-08-041-219A-6	Sequence 6, Appl
35	329	18.5	359	1	US-08-417-122-6	Sequence 6, Appl
36	327.5	18.4	395	1	US-08-476-000-2	Sequence 2, Appl
37	327.5	18.4	395	1	US-08-472-840-2	Sequence 2, Appl
38	327.5	18.4	395	1	US-08-476-976-2	Sequence 2, Appl
39	327.5	18.4	395	2	US-08-474-410-2	Sequence 2, Appl
40	327.5	18.3	395	3	US-08-486-673B-2	Sequence 2, Appl
41	325.5	18.3	395	4	US-08-486-673B-5	Sequence 5, Appl
42	325.5	18.3	399	1	US-08-476-000-61	Sequence 61, Appl
43	325.5	18.3	399	1	US-08-472-840-61	Sequence 61, Appl
44	325.5	18.3	399	2	US-08-476-976-61	Sequence 61, Appl
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ALIGNMENTS

RESULT 1	US-08-852-824-2	Application US/08852824C
Sequence 2, Applicant: Li et al.	Patent No. 6060272	GENERAL INFORMATION:
FILE REFERENCE: 1488.1220000	CURRENT APPLICATION NUMBER: US/08/852,824C	TITLE OF INVENTION: Human G-Protein Coupled Receptors
CURRENT FILING DATE: 1997-05-04	NUMBER OF SEQ ID NOS: 18	SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2	LENGTH: 342	TYPE: PRT
ORGANISM: genomic	US-08-852-824-2	
Query Match	100.0%;	Score 1778; DB 3; Length 342;
Best Local Similarity	No. 100.0%;	Pred. No. 1.3e-144;
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DB 1	MQAVDNLTSAFGNTSLCTRDYKITQVLPFLYVLFVGLITNGLAMRIFFQIRSNFT	60
OY 61	IFLKNTVSDLMILTFPEPKIISDAKLGCPRTFVCQVTSVFYFTMYTISIFLGIT	120
DB 61	IFLKNTVSDLMILTFPEPKIISDAKLGCPRTFVCQVTSVFYFTMYTISIFLGIT	120
OY 121	DRYQRTTRPFTSNPKNLGAKITLSVIAFMFLSLPMNMLTNROPDKNVKCSFLKS	180
DB 121	DRYQRTTRPFTSNPKNLGAKITLSVIAFMFLSLPMNMLTNROPDKNVKCSFLKS	180
OY 181	EGGLVWHEIVNYICQVIFMIFNLIVCYTLTKEDLYRSVTRGVGVKPKVNVKVF	240
DB 181	EGGLVWHEIVNYICQVIFMIFNLIVCYTLTKEDLYRSVTRGVGVKPKVNVKVF	240
OY 241	IIAVFFICVPHFAPRIPTLSQTRVPCDTAENTLFYKKESTLMTLSLACIDPFIYF	300
DB 241	IIAVFFICVPHFAPRIPTLSQTRVPCDTAENTLFYKKESTLMTLSLACIDPFIYF	300
OY 301	LCKSFRNLSMLKCPNSATSLSDNRKKEDGGDPNEETPM	342
DB 301	LCKSFRNLSMLKCPNSATSLSDNRKKEDGGDPNEETPM	342
RESULT 2	US-09-221-456-2	

Sequence 2, Application US/09221456
Patent No. 6162899
GENERAL INFORMATION:
APPLICANT: SATHE, GANESH
APPLICANT: HALSEY, WENDY
APPLICANT: MUIR, ALISON
APPLICANT: CHAMBERS, JON
APPLICANT: SEZERES, PHILIP
TITLE OF INVENTION: METHODS OF SCREENING FOR AGONISTS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ratner & Prestia
STREET: P.O. Box 980
CITY: Valley Forge
STATE: PA USA
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/221,456
FILING DATE: 28-DEC-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/956,975
FILING DATE: 23-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Prestia, Paul F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH-70318-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0700
TELEX: 846169
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 333 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-221-456-2

Query Match 46.3%; Score 823; DB 4; Length 333;
Best Local Similarity 48.7%; Pred. No. 4.6e-63;
Matches 154; Conservative 57; Mismatches 103; Indels 2; Gaps 1;

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77 FPKILSDAKIGTGPLRTFCQVTSVIEFTWYISISFGLITIDYOKTTRPKTSNPK 136
75 LPEKILSDSHLAPWQIRAFVCRSSVIEFTWYISISFGLITIDYOKTTRPKTSNPK 134

137 NLGAKILSVIIMAFMFLSLPNMILTRQPRDKNVKCSGLKSEGLVHWEIYNYTQV 196
135 KPVFAKTYSIFIMFLEFISLPTNLSNKEATPSSVKKCSGLKSEGLVHWEIYNYTQV 194

197 IFWINFLIIVCYTLTKELYSYVRTRGVKVPKRVNVKVFIIITAVFICVPHFAR 256
195 IFWTVEFILMLVFFVYVIAKKVDSYRKSCKDRKNNKLEGVVAVFVCFAPHFAR 254

257 IPVTLSOTRDPVCTAENLTFFYVESTLMTLSNACDPFYFLCKSEFNSLSMLKCP 316
255 VPTTHSOTNNKTCRLONOFLAKETTLFLAATNICHMDPLIYIFLCKFTKLPQMO--G 312

317 NSATSLSDNRKKEOD 332

Db 313 RKTASQENHSSQTD 328
RESULT 3
US-09-558-740-2
Sequence 2, Application US/09558740
Patent No. 6358695
GENERAL INFORMATION:
APPLICANT: SATHE, GANESH
APPLICANT: HALSEY, WENDY
APPLICANT: MUIR, ALISON
APPLICANT: CHAMBERS, JON
APPLICANT: SEZERES, PHILIP
TITLE OF INVENTION: METHODS OF SCREENING FOR AGONISTS AND
TITLE OF INVENTION: ANTAGONISTS OF THE HNEA81 RECEPTOR
FILE REFERENCE: GH-70318-2
CURRENT FILING DATE: 2000-04-26
PRIOR FILING DATE: 1997-10-23
PRIOR APPLICATION NUMBER: 09/221,456
PRIOR FILING DATE: 1998-12-28
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 333
TYPE: PRT
ORGANISM: HOMO SAPIENS
US-09-558-740-2

Query Match 46.3%; Score 823; DB 4; Length 333;
Best Local Similarity 48.7%; Pred. No. 4.6e-63;
Matches 154; Conservative 57; Mismatches 103; Indels 2; Gaps 1;

17 CTRDYKITOVLPFLYLVFVGVLTNGLAMRIFFOIRKSNFIPLKNTVSDMLMLT 76
15 CPMRTRIVQVLPFALYVVEFTGLTLMTLAWVHVPSSFTIYKNTLVADLMTLM 74

77 FPKILSDAKIGTGPLRTFCQVTSVIEFTWYISISFGLITIDYOKTTRPKTSNPK 136
75 LPEKILSDSHLAPWQIRAFVCRSSVIEFTWYISISFGLITIDYOKTTRPKTSNPK 134

137 NLGAKILSVIIMAFMFLSLPNMILTRQPRDKNVKCSGLKSEGLVHWEIYNYTQV 196
135 KPVFAKTYSIFIMFLEFISLPTNLSNKEATPSSVKKCSGLKSEGLVHWEIYNYTQV 194

197 IFWINFLIIVCYTLTKELYSYVRTRGVKVPKRVNVKVFIIITAVFICVPHFAR 256
195 IFWTVEFILMLVFFVYVIAKKVDSYRKSCKDRKNNKLEGVVAVFVCFAPHFAR 254

257 IPVTLSOTRDPVCTAENLTFFYVESTLMTLSNACDPFYFLCKSEFNSLSMLKCP 316
255 VPTTHSOTNNKTCRLONOFLAKETTLFLAATNICHMDPLIYIFLCKFTKLPQMO--G 312

317 NSATSLSDNRKKEOD 332

313 RKTASQENHSSQTD 328

RESULT 4
US-08-812-871-1
Sequence 1, Application US/08812871
Patent No. 5955303
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Guegler, Karl
APPLICANT: Muzong, Cheng
TITLE OF INVENTION: NOVEL HUMAN CHEMOKINE RECEPTOR-LIKE
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: diskette
OPERATING SYSTEM: IBM Compatible
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/812,871
FILING DATE: filed Herewith
PRIORITY APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0237 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 333 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: MML3D701
CLONE: 568987
US-08-812-871-1

Query Match 44.8%; Score 797; DB 2; Length 333;
Best Local Similarity 47.8%; Pred. No. 7,7e-61;
Matches 151; Conservative 57; Mismatches 106; Indels 2; Gaps 1;

QY 17 CTSDYKITOVLPPLTYVLFVGLITNGLAMRIFFOIRSKSNFTIFLKNVTSIDLLMT 76
DB 15 CPDRTIRIVQVLPALYVFLTGILNTLALMVFVHIPSSSTFIYLNKTLVADIMTLM 74
QY 77 FPKKILSDAKLGTGRLTFVFCQVTSVIFFTMYISISFLGLITDRQKTRPRKTSMPK 136
DB 75 LPRKILSDSHLAWQMLRAFCVCRSSVIFFTMYVIGVLLGLIADRFKILIRPLNIFLK 134
QY 137 NLGAKILSVIVAFMFLSLPNMILTNROPDRKNVKKCSFLKSEFGLVWHEIYNYICQV 196
DB 135 KPFKATVSTFVIFLFFILPIMILSNKEPTSSVKKCSLKPGLIKMHWNNNICQF 194
QY 197 IEMINFLIVICVCTLTRELRSYVTRGVGVKVRKVNKVFIIIAVFIFCFVPHFRAR 256
DB 195 IEMTVILMLVFVYVIAKKYDYSRKSKCKDRKNKKTLECKVVFVVFVFCFAPHFRAR 254
QY 257 IPTVLSOTRNVFCCTAENTLFYVKESTLMLTSLNACDPTFYFFLCKSFRRSLSMKCP 316
DB 255 VPTTHSQTNKKTCCRLONQFLIAKETTLFLAATNIMCDPLISIFLCKKFTKELPCMO--G 312
QY 317 NSATSLSDNRKKEOP 332
DB 313 RKTASSQENHSSQTD 328

RESULT 5
US-08-467-948A-29
Sequence 29, Application US/08467948A
Patent No. 5998164
GENERAL INFORMATION:
APPLICANT: LI, YI
APPLICANT: CAO, LIANG

APPLICANT: NI, JIAN
APPLICANT: GENTZ, REINER
APPLICANT: BUTT, CAROL J.
APPLICANT: SUTTON III, GRANGER G.
APPLICANT: ROSEN, CRAIG A.
TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein
TITLE OF INVENTION: Coupled Receptor GPR2
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,948A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04079
FILING DATE: 30-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1140003/EKS/KLM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 325 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-467-948A-29

Query Match 43.4%; Score 772; DB 2; Length 325;
Best Local Similarity 47.5%; Pred. No. 1e-58;
Matches 149; Conservative 60; Mismatches 105; Indels 0; Gaps 0;

QY 6 NLTSAPAGNTSLCTRDYKITOVLPPLTYVLFVGLITNGLAMRIFFOIRSKSNFTIFLKN 65
DB 2 NSTSTQPPPESSQNLITQOIIIPVLYCMVFTAGIILNVGSMIFRYVSSKSFIIYLNK 61
QY 66 TVISDLMLITPEPKILSDAKLGTGRLTFVFCQVTSVIFFTMYISISFLGLITDRYOK 125
DB 62 IYIADPVMGLTFPEPKILGDSGLGPMQANFVCRVSAVLFVNNYVSIVFGLISPDRYK 121
QY 126 TTRPKTSNPKNDLGAKILSVIVAFMFLSLPNMILTNROPDRKNVKKCSFLKSEGLV 185
DB 122 IVKPLMTSFIOSSYSKSLISVYIMMLMLLAVNIIILTNQSVREVIQKCIETKSELGRK 181
QY 186 WHEIYNYICQVEMINFLIVICVCTLTRELRSYVTRGVGVKVRKVNKVFIIIAVF 245
DB 182 WHKASNYIFVALFVIFELIVFTYITIKIFSHLKSRSNYSVKKSSRNIFSTVVF 241
QY 246 FICFVPHFRARIPYTLSDYFDCCTAENTLFYVKESTLMLTSLNACDPTFYFFLCKSF 305
DB 242 FVCFVPHFRARIPYTRKSGEHAHSCSKELRYMKKEFTLLSANVNCIDPTIYFPLCQPF 301
QY 306 RNSLISMLKCPNSA 319
DB 302 REILCKKLIHPIKA 315

RESULT 6

US-08-467-947A-29

Sequence 29, Application US/08467947A

Patent No. 6090375

GENERAL INFORMATION:

APPLICANT: LI, YI

APPLICANT: CAO, LIANG

APPLICANT: NI, JIAN

APPLICANT: GENTZ, REINER

APPLICANT: BULT, CAROL J.

APPLICANT: SUTTON III, GRANGER G.

TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein

TITLE OF INVENTION: Coupled Receptor GPR1

NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:

ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.

STREET: 1100 NEW YORK AVE., NW, SUITE 600

CITY: WASHINGTON

STATE: DC

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/467, 947A

FILING DATE: 06-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/04079

FILING DATE: 30-MAR-1995

ATTORNEY/AGENT INFORMATION:

NAME: STEFFE, ERIC K.

REGISTRATION NUMBER: 36,688

REFERENCE/DOCKET NUMBER: 1488.1140002/EKS/KLM

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 29:

SEQUENCE CHARACTERISTICS:

LENGTH: 325 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: not relevant

MOLECULE TYPE: peptide

US-08-467-947A-29

Query Match 43.4%; Score 772; DB 3; Length 325;

Best Local Similarity 47.5%; Pred. No. 1e-58;

Matches 149; Conservative 60; Mismatches 105; Indels 0; Gaps 0;

6 NLTSAGNTSLCTRDYKITOVLPFLYLVLFVGLITNGLAMRIFFOIRSKSNFIIFLKN 66

2 NSTSTQPPDESCGONLITQOIIIVLCVWFIAGILNGVSGWIFVYVSSKSFIIYLN 61

66 TVISDLMLITFPFKILSDAKLGTPRLTFCVQVTSVIFFTWYISISFLGLITIDRQK 125

62 IVIADFWMSLTFPKILGDSGLGPMQNVFVCVSAVLEFVNMVYSIVFGLISFDRIYK 121

126 TTRPFTSKNPKNLGAKILSVIWMFLLSLPMNLTNRQPDKNVKKCSFLKSEGLV 185

122 IVKPLMTSFQSVSKSLSLVIMMLLAVPNIITNOSVREVTQIKIEKSELGRK 181

186 WHEIVNYICOVIFEMINFLIVCYTLITKELYSVTRGVGKVPKKNVKKVPIIAVF 245

182 WKASNVNIFAVIFVLLIVETATIKIKFKSHKSSRSTSVKSSKNISIVFV 241

246 FICFVPHFKRIPYTLISQTRDVEPCTAENLIFYKESLMTSLNACLDPIITYFLCKSF 305

RESULT 7

US-08-988-876-8

Sequence 8, Application US/08988876

Patent No. 6063596

GENERAL INFORMATION:

APPLICANT: Lal, Preeti

APPLICANT: Bandman, Olga

APPLICANT: Hillman, Jennifer L.

APPLICANT: Yue, Henry

TITLE OF INVENTION: G PROTEIN COUPLED RECEPTORS ASSOCIATED

TITLE OF INVENTION: WITH IMMUNE RESPONSE

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/988, 876

FILING DATE: Herewith

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0441 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-855-0555

TELEFAX: 650-845-4166

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 338 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: GenBank

CLONE: 285995

US-08-988-876-8

Query Match 43.4%; Score 772; DB 3; Length 338;

Best Local Similarity 47.5%; Pred. No. 1.1e-58;

Matches 149; Conservative 60; Mismatches 105; Indels 0; Gaps 0;

6 NLTSAGNTSLCTRDYKITOVLPFLYLVLFVGLITNGLAMRIFFOIRSKSNFIIFLKN 65

3 NSTSTQPPDESCGONLITQOIIIVLCVWFIAGILNGVSGWIFVYVSSKSFIIYLN 62

66 TVISDLMLITFPFKILSDAKLGTPRLTFCVQVTSVIFFTWYISISFLGLITIDRQK 125

63 IVIADFWMSLTFPKILGDSGLGPMQNVFVCVSAVLEFVNMVYSIVFGLISFDRIYK 122

126 TTRPFTSKNPKNLGAKILSVIWMFLLSLPMNLTNRQPDKNVKKCSFLKSEGLV 185

123 IVKPLMTSFQSVSKSLSLVIMMLLAVPNIITNOSVREVTQIKIEKSELGRK 182

Query 186 WHEIVNYICGVIFWIFLIVYCYTLITKELYSYVTRGVKVPKKNVKEFIIAVF 245
183 WKKASNYIFAIFWIFLIVYCYTLITKELYSYVTRGVKVPKKNVKEFIIAVF 242
Query 246 FICFVFPFHARIPYTLISQTRDVFDCIAENTLFYVKESTLMTLSINACLDPIYFFLCKSF 303
243 FICFVFPFHARIPYTLISQTRDVFDCIAENTLFYVKESTLMTLSINACLDPIYFFLCKSF 302
Query 306 RNSLSMLKCPNSA 319
303 RELCKKHLHPLKA 316

Result 8
US-09-303-524A-2
Sequence 2, Application US/09303524A
Patent No. 6238673
GENERAL INFORMATION:
APPLICANT: CHAMBERS, JONATHAN K.
APPLICANT: STEWART, BRIAN R.
APPLICANT: AMES, ROBERT S.
APPLICANT: SARAU, HENRY M.
APPLICANT: FOLEY, JIM
APPLICANT: ARNOLD, ANNE ROMANIC
TITLE OF INVENTION: METHODS OF SCREENING FOR AGONISTS AND
TITLE OF INVENTION: ANTAGONISTS OF THE INTERACTION BETWEEN THE HUMAN KIAA0001
TITLE OF INVENTION: RECEPTOR AND LIGANDS THEREOF
FILE REFERENCE: GP50007
CURRENT APPLICATION NUMBER: US/09/303,524A
CURRENT FILING DATE: 1999-04-30
PRIOR APPLICATION NUMBER: 60/083,957
PRIOR FILING DATE: 1998-05-01
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO: 2
LENGTH: 338
TYPE: PRF
ORGANISM: Homo sapiens
US-09-303-524A-2

Query Match 43.4%; Score 772; DB 4; Length 338;
Best Local Similarity 47.5%; Pred. No. 1,1e-58;
Matches 149; Conservative 60; Mismatches 105; Indels 0; Gaps 0;

Query 6 NLTSAPGNTSLCTRDYKKTQVLEPLLYTLFVGLITNGLAMRIFFQIRSKSNFIIFLKN 65
3 NSTSTQPPDESCSQNLITQIIPVLCVMEFIAGILNGVSGMIFVYVPSKSFIIYLKN 62
Query 66 TVISDLMLITFPFKILSDAKLGTGRLRTVCOVTSVIFFTMYISISFLGLITIDRQK 125
63 IVADLVMSLTFFPKILGDSGLPQWOLNVFCVSAVLEFVNMVSVIFEFLLISFDRYK 122
Query 126 TTRPFTKSNPKNLGAKILSVIAFMFLSLPMLITRNPRDKNVKCSFLKSEFLV 185
123 IVKPLMTSFLQSVYSKLSLVYMMMLLAVPIIITNOSVREVTOIKCELSSELRK 182
Query 186 WHEIVNYICGVIFWIFLIVYCYTLITKELYSYVTRGVKVPKKNVKEFIIAVF 245
183 WKKASNYIFAIFWIFLIVYCYTLITKELYSYVTRGVKVPKKNVKEFIIAVF 242
Query 246 FICFVFPFHARIPYTLISQTRDVFDCIAENTLFYVKESTLMTLSINACLDPIYFFLCKSF 303
243 FICFVFPFHARIPYTLISQTRDVFDCIAENTLFYVKESTLMTLSINACLDPIYFFLCKSF 302
Query 306 RNSLSMLKCPNSA 319
303 RELCKKHLHPLKA 316

RESULT 9

US-08-988-876-3
Sequence 3, Application US/08988876
Patent No. 6063596
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Yue, Henry
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTORS ASSOCIATED
TITLE OF INVENTION: WITH IMMUNE RESPONSE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/988,876
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0441 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 358 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: PROSTUT09
CLONE: 1650519
US-08-988-876-3

Query Match 38.2%; Score 679.5; DB 3; Length 358;
Best Local Similarity 43.7%; Pred. No. 9e-51;
Matches 132; Conservative 64; Mismatches 99; Indels 7; Gaps 4;

Query 6 NLTSAPG-NTSLCTRDYKKTQVLEPLLYTLFVGLITNGLAMRIFFQIRSKSNFIIFLKN 64
25 NNSDGRGKRTTL--HNEDDTIVLPVLYLITFASILLNGLAVIIFPHINKKSFIIYLK 81
Query 65 NTVISDLMLITFPFKILSDAKLGTGRLRTVCOVTSVIFFTMYISISFLGLITIDRQK 124
82 NIVVADLITMTLFPFRIVADAGCPMYFELICRYTSVLEFVNMVSVIFEFLLISFDRYK 122
Query 126 TTRPFTKSNPKNLGAKILSVIAFMFLSLPMLITRNPRDKNVKCSFLKSEFLV 185
123 IVKPLMTSFLQSVYSKLSLVYMMMLLAVPIIITNOSVREVTOIKCELSSELRK 182
Query 186 WHEIVNYICGVIFWIFLIVYCYTLITKELYSYVTRGVKVPKKNVKEFIIAVF 245
183 WKKASNYIFAIFWIFLIVYCYTLITKELYSYVTRGVKVPKKNVKEFIIAVF 242
Query 246 FICFVFPFHARIPYTLISQTRDVFDCIAENTLFYVKESTLMTLSINACLDPIYFFLCKSF 303
243 FICFVFPFHARIPYTLISQTRDVFDCIAENTLFYVKESTLMTLSINACLDPIYFFLCKSF 302
Query 306 RNSLSMLKCPNSA 319
303 RELCKKHLHPLKA 316

Db 121 SLVIWAIVAASAYFLVMDSTNVVSNKAGSGNITRC--FERYEKSGKPVLIH-----IC 174
QY 195 QVI-FWNLFLVICYTLTTELRSYVRGKGVPRKKVNVKVFLLIAVEFICVPPH 253
Db 175 IYVGFVFLILLICNLVLIHTLRLGKPVKQORNAEV--RRALMVCVTAIAVFICVPPH 233
QY 254 FARIPTLSQTRDVEDCTAENTLFYVKESTLWLTSLNACLDPEFIYFELCKSFNLSLSML 313
Db 234 MVQLPMTLAEI-GMPPSSNHQAINDAHQVTLCLLSTNCVLDPVYICFLTKKFRKHLSEKL 292
QY 314 KCPNSATSLSDNKRKEDGSDPNEETPM 342
Db 293 NIMRSSQKCSRVTRDTGTETMAIPINHPPV 321

RESULT 14
PCT-US93-08528-39
Sequence 39, Application PC/TUS9308528
GENERAL INFORMATION:
APPLICANT: New York University
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08528
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY-2 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 326 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US93-08528-39

Query Match 23.1%; Score 410.5; DB 5; Length 326;
Best Local Similarity 32.2%; Pred. No. 7.7e-28;
Matches 106; Conservative 65; Mismatches 137; Indels 21; Gaps 9;

Db 1 LEPFLVTLFVGLITNGLANRIFFOI-RSKSNFI-IFLKNTVISDLMILTFPKIISD 84
QY 27 LEPFLVTLFVGLITNGLANRIFFOI-RSKSNFI-IFLKNTVISDLMILTFPKIISD 84
Db 1 LEPFLVTLFVGLITNGLANRIFFOI-RSKSNFI-IFLKNTVISDLMILTFPKIISD 84
QY 85 AKUGTGLRFRVCOVTSIFFTMTISISFLGLITIDRYQKTRFKTSNPKNLGAKIL 144
Db 61 SNOGNMFLPKFLMACGLFINTYCSVAFLGVITYNRFQAVKPIKTAQATRRKGIAL 120
QY 145 SVVW-----AFMELLSLPMILTNROPKRNKCKSELSSEG----LWHELVANIC 184

Db 121 SLVIWAIVAASAYFLVMDSTNVVSNKAGSGNITRC--FERYEKSGKPVLIH-----IC 174
QY 195 QVI-FWNLFLVICYTLTTELRSYVRGKGVPRKKVNVKVFLLIAVEFICVPPH 253
Db 175 IYVGFVFLILLICNLVLIHTLRLGKPVKQORNAEV--RRALMVCVTAIAVFICVPPH 233
QY 254 FARIPTLSQTRDVEDCTAENTLFYVKESTLWLTSLNACLDPEFIYFELCKSFNLSLSML 313
Db 234 MVQLPMTLAEI-GMPPSSNHQAINDAHQVTLCLLSTNCVLDPVYICFLTKKFRKHLSEKL 292
QY 314 KCPNSATSLSDNKRKEDGSDPNEETPM 342
Db 293 NIMRSSQKCSRVTRDTGTETMAIPINHPPV 321

RESULT 15
US-08-988-876-9
Sequence 9, Application US/08988876
Patent No. 6063596
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Yue, Henry
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTORS ASSOCIATED
TITLE OF INVENTION: WITH IMMUNE RESPONSE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/988,876
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0441 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 342 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 49443
US-08-988-876-9

Query Match 22.1%; Score 392.5; DB 3; Length 342;
Best Local Similarity 30.7%; Pred. No. 2.8e-26;
Matches 103; Conservative 66; Mismatches 146; Indels 21; Gaps 9;

Db 20 DYKITQVLEPFLVTLFVGLITNGLANRIFFOI-RSKSNFI-IFLKNTVISDLMILTN 76
Db 10 DSEFRTLEPFIYSLIFVGLITANGVLMVFAFLRPSKLNELIKITMNVNLTADVADLEFLIT 69

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